#### STIC-Siote th/ChemLib

Ford, Vanessa Thursday, October 10, 2002 5:38 PM STIC-Biotech/ChemLib In re: 09543407 Sequence seardh

Fr m: Sent: To: Subject:

Please search SEQ ID NO: 5 and please run an oligmer search on SEQ ID NO: 5.

I also need interference searches run.

Thanks!

Vanessa L. Ford **Biotechnology Patent Examiner** 

Office: CM1 8B13 Mailbox: CM1 8E12 Phone: 703.308.4735

**Edward Hart** Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

Searcher:
Phone:
Location:
Date Picked Up: 10 11 102
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA segment which encodes a foreign epitope or antigen. Also described are: segmence which aggregative fimbriae (SEFI7/TAF) nucleation depended (I) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of Farecombinate comprising recombinant Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively: (2), AgfA, CsgA and AgfA-homologue fimbria subunits, respectively: (2), homologous species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
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CC copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant comprising a replacement segment or segments of foreign complete control or sequence or sequences grown on a Salmonella, E. coli or complete comprision of recombinant with a carrier or diluent. (1) is colymer into the animal in conjunction with a carrier or diluent. (1) is colymer eliciting an immune response in an animal. In a fimbrial presentation complete 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                          WPI; 2000-672631/65
N-PSDB; AAC64622.
                                                                                                                                                                                          White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDGWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                            Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                            99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                               Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 151; DB 21
Pred. No. 3e-144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                   SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
                                                                                                                                                                                                     Kay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151;
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Recombinant agfA gene having a segment replaced by a foreign sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response

response

in animal

DNA

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PRYNTH THE TENT OF THE TENT OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising separating an amino acid polymer comprising a recombinant of AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonelia, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful consecution an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrian protein possesses both the chmunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong components the inserted epitope, and hybrid fimbriae are easy and consecution of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
26-APR-1994;
                                                                  26-APR-1993;
                                                                                                                                     03-JUN-1997
                                                                                                                                                                                                       US5635617-A.
                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis 27655-3b agfA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW23570 standard; Protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a recombinant agfa gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segmence which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNAALVN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNAALVN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                        enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
94US-0233788
                                                                  9305-0054452
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                       /note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 127; DB 21; I
Pred. No. 4.8e-120;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 151;
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RESULT 5
AAB36347
ID AAB3
Вþ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can be used to provide proteins and antibodies which can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family
            White AP,
                                                                 05-APR-1999;
                                                                                         05-APR-2000; 2000WO-CA00356
                                                                                                                                             WO200060102-A2
                                                                                                                                                                     Synthetic
                                                                                                                                                                                                 Salmonella enteritidis
                                                                                                                                                                                                                           vaccine;
                                                                                                                                                                                                                                     Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                 AgfA::PT3#2 amino acid sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                           26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                AAB36347 standard; Protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virtually all other microbial organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 7; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYVI-) UNIV VICTORIA INNOVATION & DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1993;
                                     (UYVI-) UNIV VICTORIA.
                                                                                                                   12-OCT-2000
                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                         121 NN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKLLKVAAFAATVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                          immune response;
           Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                          (first entry)
                                                               99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0054452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.8%; Score 122; DB 18; 100.0%; Pred. No. 5.3e-115;
            Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SK,
                                                                                                                                                                                                                           immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC segment of the gene has been replaced by a segment of a foreign DNA CC segment of thin aggregative fimbriae (SEFIT/TAP) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and depended CC assembly system of strains of Salmonella, Escherichia coli and combinant CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) the chomologous species; (3) directing recombinant gene into the chromosome of the chomologous species, replacing the native back into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant comprising a recombinant comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or a salfa protein containing a replacement segment or segments of foreign cuseful for the expression of recombinant AgfA protein which is useful comprising an immune response in an animal. In a fimbrial presentation cystem the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to combinant the heterologous antigens are protein possesses both the immunogens, which may be important for directing an immune response capainst the inserted epitope, and hybrid fimbria are casally strong consequences which may be important for directing an immune response capainst the inserted epitope, and hybrid fimbriae are easy and consequence is given in the present sequence is given in the protein of the present invention.
                                                                                                                                                                                                                                                                                                                                                      RESULT 6
AAB36348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-672631/65.
N-PSDB; AAC64623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                       AgfA::PT3#3 amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                      AAB36348 standard; Protein; 151
                                                                                                                              Salmonella enteritidis
                                                                                                                                                                                    Salmonella; agfA; chromosomal gene replacement;
                                                                                         Synthetic.
                                                                                                                                                                  vaccine;
                                                                                                                                                                                                                                                             26-FEB-2001
                 12-OCT-2000
                                                     WO200060102-A2
                                                                                                            Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                               118;
                                                                                                                                                                    immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139pp; English.
                                                                                                                                                                        immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 118;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                 NO:16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .7e-111;
                                                                                                                                                                                             fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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The present invention describes a recombinant agfA gene (I) where a company of the gene has been replaced by a segment of a foreign DNA company of thin aggregative fimbriae (SEF1/T/TAF) nucleation depended company system of strains of Salmonella, Escherichia coli and company system of strains of Salmonella, Escherichia coli and company system of strains of salmonella, Escherichia coli and company of the production of fimbriae comprising recombinant coli and company of the composition of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene composition of the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant comprising separating an amino acid polymer comprising a recombinant comprising sequence or sequences grown on a Salmonella, E. coli or composition containing a replacement segment or segments of foreign containing and admining a replacement segment or segments of foreign containing and and an animal. In a fimbrial presentation containing a segment or segments of the containing and an animal in containing a replacement segment or segments of the containing and an animal in a segment or segment or segme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAC64624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                   against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention.
                                                                                                                                                immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-672631/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Doran JL,
      151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kay WW;
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RESULT 7
AAR62761
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 OS XXX DE XX
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                          AAR62761 standard; Protein; 120
                                                                                     AAR62761;
Salmonella enteritis 27655-3b
                    Salmonella; AgfA; vaccine
                                          AgfA sequence
                                                                26-JUN-1995
                                                                                                                                                                 99
                                                                                                                                                                                    99
                                                                                                                                                                                                          39
                                                                                                                                                                                                                               39
                                                                                                                                                                           NATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                         SGPDSTLSTYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFR 98
                                                                                                                                                                                                                   SGPDSTLSIYOYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFR 98
                                                                                                                                                               NNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
                                                                                                                                                                                                                                                      113;
                                                                                                                                                                                                                                                     Conservative
                                                                 (first entry)
                                                                                                                                                                                                                                                                74.8%;
                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                               Score 113; DB 21;
Pred. No. 6.3e-106;
                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                             Length 151;
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                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents the Salmonella enteritis 27655-3b TnphoA mutant strain AgfA protein. The encoding DNA and isolated AgfA protein are used in genetic immunization and vaccine compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans.
                          Clouthier SC,
                                                                26-APR-1994;
26-APR-1993;
                                                                                           26-APR-1993;
                                                                                                              03-JUN-1997.
                                                                                                                                                 Salmonella enteritidis
                                                                                                                                                                   Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                       Salmonella
                                                                                                                                                                                                          29-SEP-1997
                                                                                                                                                                                                                            AAW23569
                                                                                                                                                                                                                                             AAW23569 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig7A; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eliciting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09425598-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-358275/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KING/) KING J.
(UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-APR-1994;
                                             (UYVI-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fimbrial type proteins.
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                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                               82
                                                                                                                                                                                                                                                                                                                                       22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                                                                                                                                  سر
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
        1997-309886/28
                                                                                                                                                                                                                                                                                          VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                                                                                                                                                                                                                      112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ73066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an immune response to Salmonella -
                                                                                                                                                                                       enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                          120 AA;
                                                                                                                                                                                                                                                                                                                                                                    74.2%;
ilarity 100.0%;
Conservative
                                            VICTORIA INNOVATION & DEV CORP
                                                                                                                                                                                                       (first entry)
                          Collinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collinson SK,
                                                               94US-0233788
93US-0054452
                                                                                          9305-0054452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0054452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-IB00207
                                                                                                                                                                                    27655-3b TnphoA mutant agfA fragment
                          SK,
                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                             Score 112; DB 15;
Pred. No. 5.2e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doran JL,
                         Doran JL,
                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ella - using
or compsns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kay WW;
                         Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                      Length 120;
                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                     0
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RESULT 9
AAB36352
CCC XXX PFF FF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents an agfA fragment encoded by an agfA gene fragment derived from Salmonella enteritidis 27655-3b TnphoA mutant strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are
                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in
                                                                                                                              WPI; 2000-672631/65
                                                                                                                                                    White AP,
                                                                                                                                                                                                     05-APR-1999;
                                                                                                                                                                                                                          05-APR-2000;
                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                            Salmonella enteritidis
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                        Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated Salmonella gene agfa - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family
                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                  12-OCT-2000
                                                                                                                                                                                                                                                                         WO200060102-A2
                                                                                                                                                                                                                                                                                                                                               vaccine;
                                                                                                                                                                                                                                                                                                                                                                                 AgfA::PT3#7 amino acid sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36352 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2;
                                                                                                                                                                            (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity
112; Conserv
                                                                                                                  AAC64628
                                                                                                                                                                                                                                                                                                                                               immune
                                                                                                                                                   Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                           2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                   99US-0127888
                                                                                                                                                                                                                                                                                                                                              response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.28;
                                                                                                                                                    Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                              immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 112;
Pred. No.
                                                                                                                                                    SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                    Kay
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                                                                                                                                                                                                                                                                                                                                                                                  NO:24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.2e-105;
                                                                                                                                                    ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                  in animal
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The present invention describes a recombinant agfA gene segment of the gene has been replaced by a segment of a

(I) where a foreign DNA

Disclosure; Page 138; 139pp; English.

sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response

immune response in animal

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Coopy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant of AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or amino acid sequence or sequences grown on a Salmonella, E. coli or contract of the animal in conjunction with a carrier or diluent. (I) is colymer into the animal in conjunction with a carrier or diluent. (I) is conjunction to the expression of recombinant AgfA protein which is useful conjunction with a carrier or diluent. (I) is conjunction to the expression of recombinant AgfA protein which is useful conjunction an eliciting an immune response in an animal. In a fimbrial presentation conjunction to the hybrid fimbrin protein possesses both the compose (vaccine, the carrier fimbrial subunit proteins are usually strong conjunction, which may be important for directing an immune response conjunction the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
AAB36355
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  В
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB36355 standard; Protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#10 amino acid sequence SEQ ID NO:30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-2001
                                                                                                                                                                                                                                   05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis
                                                                                                                                                                                         05-APR-1999;
                                                                                                                                                                                                                                                                             12-OCT-2000
                                                                                                                                                                                                                                                                                                                       WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine;
Recombinant agfA gene having
                                         WPI; 2000-672631/65.
N-PSDB; AAC64631.
                                                                                                                                                 (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                            Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                              99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.8%;
                                                                                                                Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                  SK,
           segment replaced by a foreign
                                                                                                                  Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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comprising separating an amino acid polymer comprising a recombinant comprising separating an amino acid polymer comprising a recombinant comparising acid sequence or sequences grown on a Salmonella, E. coll or comprising a recombinant comprising a recombinant. (I) is comprised for the expression of recombinant against in a fimbrial presentation comprising an immune response in an animal. In a fimbrial presentation comprised comprises/cell), the hybrid fimbrin protein possesses both the comprise comprises/cell), the hybrid fimbrin protein possesses both the comprise comprises relevant for an efficient live immunogens, which may be important for directing an immune response comprises the inserted epitope, and hybrid fimbriae are easy and comprised to purify in large amount. The present sequence is given in compensive to purify in large amount. The present sequence is given in compressive to purify in a present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEPI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of salmonella, Escherichia coli and AgfA, CsgA and AgfA-homologue fimbriae subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 139; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                exemplification of the present invention.
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              δÃ
                                  dd
                                                                    Matches
                                                                            Best Local
                                                                                   Query Match
                                                                                                      Sequence
                 61
 61
                                   \vdash
                                                    -
                                   MKLLKVAAFAATVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSTYQYGSANAALALQ
                                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
Similarity 100.
02; Conservative
                                                                                67.5%;
100.0%;
                                                                       0;
                                                                                Score 102;
Pred. No.
                                                                       Mismatches
                                                                                 ; DB 21;
. 7.8e-95;
                                                                                          Length 151;
                                                                           0;
                                                                           Gaps
                                          60
                                                           60
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0

QΥ

151 AA;

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RESULT 11
AAB36349
                                                                                                                                                                                 AAB36349 standard; Protein; 151 AA
                                                                                                               Salmonella; agfA; chromosomal gene replacement;
                                                                                                                                                                  AAB36349;
                                                                               Salmonella enteritidis
Escherichia coli
                                                                                                                                AgfA::PT3#4 amino acid sequence SEQ ID NO:18
                                                                                                                                                26-FEB-2001
                      05-APR-2000; 2000WO-CA00356
                                                                       Synthetic
                                                                                                        vaccine; immune
       05-APR-1999;
                                        12-OCT-2000
                                                       WO200060102-A2
                                                                                                                                                 (first entry)
         99US-0127888
                                                                                                          response;
                                                                                                            immunogen
                                                                                                                      fimbrin; epitope;
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(UYVI-) UNIV VICTORIA.

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RESULT 12
AAB36351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and the exemplification of the present sequence is given in the present sequence is given in
               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA. CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-672631/65.
                                                     Salmonella enteritidis
                                                                                                           Salmonella; agfA; chromosomal gene replacement;
                                                                                                                                                 AgfA::PT3#6
                                                                                                                                                                                                                                                              AAB36351 standard; Protein; 151
                                   Escherichia coli
                                                                                           vaccine;
                                                                                                                                                                                      26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                               118
                                                                                                                                                                                                                                                                                                                                                                                                 118 YGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                         88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                                                                                                                                                                                             YGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                       ALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQ 117
                                                                                         immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
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                                                                                                                                               amino acid sequence SEQ ID NO:22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u></u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.3%; Score 94;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collison
                                                                                           1mmunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                  B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21; L
. 9.1e-87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 151;
                                                                                                           fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       depended
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RESULT 13 AAB36354

DXXXXX

26-FEB-2001

(first entry)

AAB36354;

AAB36354 standard; Protein;

151

AgfA::PT3#9 amino acid sequence SEQ ID NO:28

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                                                                               В
                                                                                                                   Ωy
                                                                                                                                                                                                                                             cc directing recombination of a recombinant gene into the chromosome of the chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native cc back into the chromosome of the homologous species, replacing the native cc copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign camino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the colymer into the animal in conjunction with a carrier or diluent. (1) is cuseful for the expression of recombinant AgfA protein which is useful cor eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are bresented in high numbers (up to 500,000 copies/cell), the hybrid fimbrial protein possesses both the carrier fimbrial subunit proteins are usually strong the immunogenes which may be imported for the subunit proteins are usually strong.
                                                                                                                                                             Matches
                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichla coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                   immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-672631/65.
N-PSDB; AAC64627.
                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 137; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-1999;
                                     61
61 SDARKSETTITQSGYGNGADVGQGADN 87
                                                                             exemplification of the present invention
                    SDARKSETTITQSGYGNGADVGQGADN
                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doran JL,
                                                                                                                                                                                                                                             151 AA;
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0127888
                                                                                                                                                                              57.6%;
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                                                                                                                                                             0;
                                                                                                                                                                                Score 87;
Pred. No.
                                                                                                                                                           Mismatches
                                     87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay WW;
                                                                                                                                                                              DB 21;
. 1e-79;
                                                                                                                                                             0
                                                                                                                                                                                                Length 151;
                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                   is given
                                                                                                                                                         Gaps
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cc segment of the gene has been replaced by a segment of a foreign DNA cc sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended cc assembly system of strains of Salmonella, Escherichia coli and cd interobacteriaceae for the production of fimbriae comprising recombinant cc AgfA, CsgA and AgfA-homologue fimbria subunits, respectively: (2) cc AgfA, CsgA and AgfA-homologue fimbria subunits, respectively: (2) cc AgfA, CsgA and the chromosome of the fimbriae comprising recombinant cc copy of that gene; and (4) eliciting an immune response in an animal, cc comprising separating an amino acid polymer comprising a recombinant cc apida protein containing a replacement segment or segments of foreign cc AgfA protein containing a replacement segment or segments of foreign cc polymer into the animal in conjunction with a carrier or diluent. (1) is coll greateful for the expression of recombinant AgfA protein which is useful cc system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrian protein possesses both the cc immunogenicity and adhesion properties relevant for an efficient live capainst the inserted epitope, and hybrid fimbriae are easy and consensive to purify in large amount. The present sequence is given in the hybrid fimbriae are easy and consensive to purify in large amount. The present sequence is given in the memphisication of the present invention.
                              Qy
                                                                  В
                                                                                              δÃ
밁
                                                                                                                                  Query Match
Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                      Sequence
                              61 SDARKSETTITQSGYGNGAD
 61
                                                                                                    \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-672631/65
DB; AAC64630.
                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                    MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
 SDARKSETTITQSGYGNGAD
                                                                                                                                    l Similarity
80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Doran JL,
                                                                                                                                                                                                          151 AA;
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0127888
                                                                                                                                                        53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collison SK,
                                     80
                                                                                                                                         score 80; DB; pred. No. 1.2
0; Mismatches
                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay WW;
                                                                                                                                           DB 21; I
. 1.2e-72;
ches 0;
                                                                                                                                                                           Length 151
                                                                                                                                               Indels
                                                                                                                                               0;
                                                                                                                                                 Gaps
                                                                                                                                                 0;
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RESULT 14,

QΥ

74 GYGNGADYGQGADNSTIELTQNGFRNNATIDQWNAKNSDITYGQYGGNNAALVNQTASDS 133

Matches Query Match Best Local

Similarity

51.7%;

Score 78; pred. No. Mismatches

DB 21, 5. 1.2e-70; 0;

0;

Gaps

0;

Length 151

Conservative

0;

Sequence

151 AA;

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AAB36353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36353 standard; Protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB36353;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (1) where a segment of the gene has been replaced by a segment of a foreign DNA segment which encodes a foreign epitope or antigen. Also described are: sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and assembly system of strains of salmonella, Escherichia coli and assembly system of the production of fimbriae comprising recombinant Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) AgfA, CsgA and AgfA-homologue fambria subunits the chromosome of the directing recombinant gene into the chromosome of the homologous species; (3) directing recombinant on of a recombinant gene homologous species; (3) directing recombinant on of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; immune response; immunogen
                                                                                                                                           comprising separating an amino acid polymer comprising separating an amino acid polymer copy of the acid sequence of the host cell, from the patient of the mative comprising separating an amino acid polymer comprising a recombinant comprising separating an amino acid polymer comprising a recombinant agif protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or amino acid sequence or sequences grown on a Salmonella, E. coli or control the animal in conjunction with a carrier or diluent. (I) is polymer into the animal in conjunction with a carrier or diluent. (I) is golymer into the expression of recombinant AgfA protein which is useful useful for the expression of recombinant AgfA protein which is useful useful for eliciting an immune response in an animal. In a fimbrial presentation for eliciting an immune response in an animal. In a finbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong the protein and the carrier fimbrial subunit proteins are usually strong the immunogens, which may be immortant for directing an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA seguence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2000; 2000WO-CA00356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 138; 139pp; English.
                                                immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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74

GYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133

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                     CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant CC AgfA protein containing a replacement segment or segments of foreign CC amino acid sequence or sequences grown on a Salmonella, E. coli or CC enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful CC for eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to CC 500,000 copies/cell), the hybrid fimbria protein possesses both the CC ummunogens, which may be important for directing an immune response CC against the inserted epitope, and hybrid fimbriae are easy and CC inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                 back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                                                                                       directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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N-PSDB; AAC64626.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; immune response; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AgfA::PT3#5 amino acid sequence SEQ ID NO:20
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               exemplification of the
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               present invention
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Best Local Similarity
Matches 70; Conserv
                142 FGNNATANQY 151
142 FGNNATANOY 151
                               Conservative
                                                                           46.4%; Score 70;
100.0%; Pred. No.
                                                                    0;
                                                                    Mismatches
                                                                           DB 21; I
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Search completed: October 11, 2002, 21:19:04 Job time: 34 secs

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Result
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Perfect score:
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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US-07-851-976B-8
US-08-291-609-8
US-08-401-136-8
US-08-850-554-8
US-08-934-846-4
US-08-934-846-2
US-08-934-846-2
US-08-934-846-2
US-09-238-557-2
US-08-477-346-97
US-08-473-089-97
US-08-461-9908-10
US-09-085-761A-66
US-09-085-761A-66
US-09-085-761A-66
US-09-085-761A-66
US-08-910-856-82
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US-08-910-856-82
US-09-025-7698-373
US-09-025-7698-383
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(without alignments)
216.957 Million cell updates/sec
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re 122; DB ed. No. 1.1 Mismatches	A COMPOSITIONS A 701 Fifth Av 70, Version # 788A 3.403C2	ALIGNMENTS	84-596A-45 58-731-45 84-923A-45 84-923B-20 84-158B-20 84-158B-20 84-158B-20 84-158B-20 84-158B-20 84-158B-20 84-158B-20 84-158B-20 84-158B-20 10-18-20 1
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Gaps			45, App 45, App 20, App 314, App 314, App 314, App 314, App 316, App 316, App
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Black, Michael

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RESULT 3
US-08-858-207A-291
; Sequence 291, Application US/08858207A
; Patent No. .$348328
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                         Matches
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TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: line
VOLECUIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Collinson, Karen S.
APPLICANT: Clouthler, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
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Local Similarity 100.0%; Pred. No. 5.9e-10
les 112; Conservative 0; Mismatches
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                                                                                                                                                                                                          22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NN 122
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                                                                                                                                       GOGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                                                                       VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 60
                                                                                                                     GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 112
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5. 5635617
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98104-7092
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Kay, William W.
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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N: 435
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                Sequence 8,
                                                                                                                                                                                                                                   GENERAL INFORMATION:
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APPLICATION NUMBER: US,
FILING DATE: 09-MAY-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                                            APPLICANT:
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                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                TITLE OF INVENTION:
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                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM COMPERATING SYSTEM:
SOFTWARE: FastSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                           13 NAALALQ 19
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                                                         STREET:
                                                                       ADDRESSEE:
             COUNTRY:
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94104-2675
                                           Palo Alto
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                           California
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VENTION: No. 6348328el Compounds
EQUENCES: 552
                                                         755 Page Mill Road
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Knowles, David
Nicholas, Richard
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                                                                                                               BOONMAN, JOHANNES C.P.
VENTION: CLONING AND EXPRESSION OF ACETYL XYLAN
VENTION: ESTERASES FROM FUNGAL ORIGIN
                                                                                                                                                                                        Van Den Broeck, Henriette
                                                                                                                                                                                                          Visser, Jacob
                                                                                                                                                                             Strozyk, Francois
                                                                                                                                                                                                                        De Graaff, Leendert H
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                 USA
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                                                                        Morrison
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09-MAY-1997
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                                                                        Foerster
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Pred. No.
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COMPUTER READABLE FORM:

MEDIUM TYPE:

loppy disk

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

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RESULT 5
US-08-291-609-8
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NATA:
APPLICATION NUMBER: US/08/291,609
FILING DATE: 17-AUG-1994
CLASSIFICATION NUMBER: 07/851,976
PRIOR APPLICATION NUMBER: 07/851,976
APPLICATION NUMBER: 07/851,976
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MUTAShige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 246152003200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
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NAME: MUTAShige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2461
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                                                                                                 ZIP: 94104-2675
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VENTION: CLONING AND EXPRESSION OF ACETYL XYLAN
VENTION: ESTERASES FROM FUNGAL ORIGIN
                                                                                                                                                                                                                                                                                                                                                                       USA
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Strozyk, Francois
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115 HNGGGNS 121

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Query Match
Best Local Similarity
Thehas 7; Conserv
                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-401-136-8
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SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,136
FILING DATE: 08-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTASShige, Kate H.
NAME: MUTASSHIGE, Kate H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 887-0764
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MEDIUM TYPE: Floppy disk
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 32 HNGGGNS 38
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STREET: 2000 PENNSYLVANIA AVENUE NW, SUITE 5500
CITY: Washington
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TELEX: 90-4030
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VENTION: A METHOD TO ALTER THE PROPERTIES OF
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                            4.6%; Score 7; DB llarity 100.0%; Pred. No. 33 Conservative 0; Mismatches
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100.0%;
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Pred. No.
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                                            DB 1;
o. 33;
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                              Indels
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                           Gaps
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RESULT 7
US-08-850-554-8
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                                                                                                                                                                                                                                                                                                             Sequence 4, Application Patent No. 5882898 GENERAL INFORMATION:
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Matches 7; Conserv
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ZIP: 20006-1880
COMPUTER READABLE FORM:
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: FORM:
MEDIUM TYPE
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: A METHOD TO ALTER THE PROPERTIES OF
TITLE OF INVENTION: ACCTYLATED XYLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 08-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              APPLICANT: Pearson, Stewart C.
APPLICANT: Greenwood, Rebecca C.
TITLE OF INVENTION: NOVEL folc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELECUTAL: (202) (202) (202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 HNGGGNS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2000
CTTY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 02-MAY-1997
CITY: : Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 HNGGGNS 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Murashige, Kate
REGISTRATION NUMBER: 2
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                                                                       STREET:
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                                                                                                    ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                 Application US/08934846
                                                                    E: Dechert Price & Rhoads
4000 Bell Atlantic Tower, 1717 Arch Stre
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Strozyk, Francois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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100.0%; Pred. No.
tive 0; Mismatc
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6165472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4,
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SEQUENCE CHARACTERISTICS:
LENGTH: 407 amino acids
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APPLICATION NUMBER:
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KEGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL FOLC NUMBER OF SEQUENCES: 4
                                                   ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,
                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Pearson, Stewart C. APPLICANT: Greenwood, Rebecca
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COMPUTER: I
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                                                                                                                                                                                                                 COMPUTER: IBM CONTROL OPERATING SYSTEM:
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CTTY: Philadelphia
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                                                                                                 FILING DATE:
                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                    COUNTRY: U
ZIP: 19103
                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                    SD
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RESULT 11
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                                                                                                                                    Query Match
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                                                                                                        Matches
                                                                                                                      Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
COMPUTER: DS SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pearson, Stewart C. APPLICANT: Greenwood, Rebecca
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                                            253 NAALALQ 259
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                                                             54 NAALALQ 60
                                                                                                                                                                                            LENGTH: 418 amino
TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/934,846 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 407 amino acids TYPE: amino acid STRANDEDNESS: single
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4000 Bell Atlantic Tower, 1717 Arch Stre
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linear
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                                                                                                                     4.6%; Score 7; DB 2
100.0%; Pred. No. 44;
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Pred. No. 43;
                                                                                                      Mismatches
                                                                                                                                   DB 2;
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                                                                                                                                 Length 418;
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US-08-190-802A-97
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                                                                                                                                                                                                                                                                             Sequence 97, Application US/08190802A Patent No. 5519003
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS
                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
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PRIOR APPLICATION DATA:
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OPERATING SYSTEM: DOS
SOETWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pearson, Stewart C.
APPLICANT: Greenwood, Rebecca
TITLE OF INVENTION: NOVEL folo
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                             APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Dickinson, Todd Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                253 NAALALQ 259
                                                                                                                                                                                                                                                                                                                                                                                                54 NAALALQ 60
                                                                STATE: CA
COUNTRY: USA
ZIP: 94306-0850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4000 Bell .
CITY: Philadelphia
STATE: PA
                                                                                                  CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/238,557
                                                                                                                                STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                E: Dehlinger & Associates P.O. Box 60850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Dechert Price & Rhoads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418 amino acids
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 compatible
PC-DOS/MS-DOS
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100.0%; Pred. No.
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Best Local Similarity
Thes 6; Conserve
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US-08-477-346-97
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE: INDIVIDUAL ISOLATE: CDC4 / CDC20 protein rIV, Fig. 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-0880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mochly-Rosen, Daria APPLICANT: Ron, Dorit
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ANTI-SENSE:
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                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/48
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: WD-40 -
                                                                               REFERENCE/DOCKET NUMBER: 2550-0025.20 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 01-FEB-1994
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                                                                                                                                    REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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amino acid
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                   29 amino acids
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100.0%; Pred. No. 35
Live 0; Mismatches
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US-08-473-089-97
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Patent No. 6342368
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Best Local Similarity
Matches 6; Conserv
                                                   Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                    TELEFAX: (202) 887-07 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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APPLICANT:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                     ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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TELEPHONE: (202) F
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CITY: Washington
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ZIP: 20006-1812
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15 IVVSGS 20
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                          12 IVVSGS 17
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2000 Pennsylvania Avenue,
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887-0763
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100.0%;
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RESULT 15 US-09-053-197A-61

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Sequence 61, Application US/09053197A

PATELICANT: Melinar, Joel H.

APPLICANT: Wellinar, Joel H.

APPLICANT: Melinar, Joel H.

MUMBER OF SEQUENCES: 72

COMPRESSEE: Mediam & Carroll, LLP

STREET: 200 Montsomery Screet, Suite 2200

CITY: San Francisco

COMPTER SADABLE FORM:

COMPTER SADABLE
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Result
No.
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Maximum DB seq length: 2000000000
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Perfect score:
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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length DB
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Gapop 60.0 , Gapext 60.0
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151
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Qy	Оy	Qy Db	Que Bes Mat	F; 1-2 F; 21-	A; Gene: C; Funct A; Descr A; Note: C; Keywo	A; Statu A; Molec A; Resid A; Note: C; Genet	A; Ref	A; Not R; Col J. Ba	A; Mol A; Res A; Exp	A; Res A; Cro A; Acc	A; Title: A; Refere A; Access	C; Acc R; Col	36 23 31		4444	· w 4 4 .	ս ա ա	ա ա ա	ພ ພ ພ
121 NN	61 SE 11 61 SE	1 1 M	ry Matc t Local ches 1	0/Domain 151/Prod	Gene: agra Function: Description Note: fimbr Keywords: f	F. F. R.	Reference Contents:	Note: the authors tra Collinson, S.K.; Emod Bacteriol, 173, 4773	Molecule t Residues: Experiment	;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	Title: Sal Reference Accession:	Accession: JC6039 Collinson, S.K.;	1 n pro ies: : 31		<i>α</i> ω 4 τυ	1000	20 7 60	ω 4 ro	210
	DARKSE'	MKLLKVAAFAA            MKLLKVAAFAA	57,67	uct	: ma iae imbr	elimi ype: 21-33 ence	number: 27655	autho S.K. 173	type:   21-52	1-151 1-151 rence	Salmonella ce number: on: JC6039	JC6039 S.K.; 178	otein agi Salmonel -Dec-1998		677	777	777	777	7
NNAALVNQTASDSSVMVRQVGFGNNATANQY	ETTITQSGYGNGADVGQGADNST	MKLLKVAAFAAIVVS              MKLLKVAAFAAIVVS	Similarity l; Conserva	al s imbr	D H	nary protein CO3> extracted	r: A4489	rs trans; Emody,	protein 2 <co2> burce: s</co2>	DNA 1 <col/> es: GB:U4 015	la ente r: JC60		gfA precur ella enter 96 #seguen			444			
VMVRQV	YGNGAD        YGNGAD	SGSALAGVVPQWGGGG 	100. 100. tive	equence in prote	component d to fibror	ed from	98; MUID:913105	7	in	43280;	ritidi 39; MU	015; A hier, 67 19	A precursor - : la enteritidis #sequence_rev		51 82 35		85 87	5 3 6 8 6	13 16
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	TIDQWNAI	2 - 2	. 6	d <sig> experimenta</sig>	imbria Cissue	42- UT	ayy	idue		AAC43		ser,	idis #text						
	IDQWNAKNS           IDQWNAKNS	SIYOYG	Length Indel	nta	ria ue j	936	aygregar	1		599	thin,		i e						
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major curlin chain precursor [imported] - Salmonella enterica subsp. enterica serovar Ty C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: A10635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Title: Complete genome sequence of a multiple drug resistant
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R;Parkhill, J.; Dougan, G.; James,
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N;Alternate names: csgA protein; major curlin protein
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence revision 20-Feb-1998 #text_change
C;Accession: S70788; G64846; S31202; S34560; S34559
C;Accession: S70788; G64846; S31202; S34560; S34560
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                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: EMBL:x90754; NID:gl147558; PIDN:CAA62282.1; PID:gl147564
A;Experimental source: strain K12, substrain W3110
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Recession: G64846
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A; Residues: 1-151 <PAR>
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                                                                          A; Residues: 1-151 <BLAT>
A; Residues: 1-151 <BLATOA; Residues: 1-151 <BLETOA; Residues: 1-151 <BLETOA; Residues: 1-151 <BLETOA; R. Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; A; Experimental source: strain K-12, substrain MG1655
A; Experimental source: strain MG1655
A; Expe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-151 <HAM>
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                                  Mol.
                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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Microbiol.
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                                             Arnqvist, A.; Hammar, M.;
ol. 7, 523-536, 1993
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ilarity 100.0%;
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Pred. No. 1.3e-146;
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C; Species: Escherich C; Date: 16-Feb-2001 C; Accession: H85665 R; Perna, N.T.; Plunk iller, L.; Grotbeck,

Grotbeck,

E.J.; Davis,

16-Feb-2001 #sequence\_revision 16-Feb-2001

Plunkett III, G.; Burland, V.; Mau, B.; Glasner,

N.W.; Lim,

Α.;

J.D.; Rose, Potamousis, 14-Sep-2001

K.; A

Apoda

al protein csgA [imported] -Escherichia coli

Escherichia

coli (strain 0157:H7, substrain

#text\_change

hypothetical H85665 RESULT

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A;Reference number: S34559
A;Accession: S34559
A;Molecule type: DNA
A;Residues: 1-133;/RODSGWLW' <OLS3>
A;Cross-references: EMBL:L04979; NID:g290424; PIDN:AAA23616.1; PID:g290425
A;Experimental source: strain K-12, substrain W3110
C;Genetics:
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A;Accession: S31202
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A; Residues: 1-6,'V',8-151 <OLS1>
A; Cross references: EMBL:L04979
A; Accession: S34560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: major component of wild-type curli; interaction between CsgA and CsgB A;Note: curli are thin, coiled fibers expressed on the surface of Escherichia coli th and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-20/Domain: signal sequence #status predicted <SIG>F;21-151/Product: curlin #status experimental <MAT>
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A; Residues: 21-42;44-50 <OLS2>
R; Olsen, A.N.; Arnqvist, A.M.
                                                                                                                                                                                                                                                                                                                                                                                  curlin major subunit CsgA [imported] - C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision C;Accession: D90806 R;Hayashi, T.; Makino, K.; Ohnishi, M.;
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C; Function:
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                                                                                                                                                                       A;Status: Paralland A;Status: PID: 913360880; A;Nolecule type: DNA A;Residues: 1-152 <HAY> A;Residues: 1-152 <HAY> A;Cross references: GB:BA000007; PIDN:BAB34843.1; PID:913360880; A;Cross references: Strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: csgA
                                                                                                                                                                                                                                                                                    DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D90806
A;Accession: D90806
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                                      SGSALAGVVPQ
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(asunaga, T.; Kuhara, S.; Shiba, T.; Hattori,
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C:Accession: T36490
R:Saunders, D.C.; Harris, D.; James, K.D.; Parkhill R:Saunders D.C.; Harris, D.; James, K.D.; Parkhill submitted to the EMBL Data Library, July 1999
A;Reference number: Z21608
A;Accession: T36490
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                               R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch: Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Suna Res. B. 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal-Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                            A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AF1813
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C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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T36490
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85665
                                                                                                                                                                                                  A; Reference number: AB1807; A; Accession: AF1813
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hypothetical protein alr0054 [imported] - Anabaena sp. (strain PCC 7120)
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A; Residues: 1-152 <STO>
A; Residues: 1-152 <STO>
A; Cross-references: GB:AE005174; NID:g12514574; PIDN:AAG55788.1;
A; Experimental source: strain O157:H7, substrain EDL933
                                                                            A;Gene:
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11; Conserv
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Similarity 100.0%
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Pred. No. 5;
0; Mismatches
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T34611
                 C;Accession: D89920
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
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A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus
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                                                                                                                                                                                    RESULT 10
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A;Gene: nuoN; SCOEDB:SC10A7.08c
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C;Keywords: membrane-associated complex; NAD; oxidored
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                                                                                                                                                                    A; Experimental source: strain A3(2) C; Genetics:
                                                                                                                                                                                                                                                                                                      R;Seeger, K.; Harris, D.; James, K.D.; Parkhill, submitted to the EMBL Data Library, July 1999 A;Reference number: 221598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 [similarity] - Streptomyces C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-May-2000
                                                                                                                                                                                                         A;Cross-references: EMBL:AL096837; PIDN:CAB48911.1; GSPDB:GN00070;
                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-62 <SEE>
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein SCF43A.24c - Streptomyces coelicolor
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A; Residues: 1-552 <SAU>
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Pred. No.
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N315

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A;Reference number: A897
A;Accession: D89920
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-145 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Jan-2000
C;Accession: I48605
                                                                                                                                                                                                                                                                                                      C;Accession: AH2344
C;Accession: AH2344
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOI. Cell. Endocrinol. 104, 57-66, 1994
A;Title: cDNA cloning and mRNA expression of the six mouse insulin-like growth factor bi A;Reference number: I48600; MUID:95121750
A;Accession: I48605
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2344
                                                                                                                                                                                                                                                                                                                                                                                ATP-binding protein of ABC transporter alr4311 [imported] - Anabaena sp. (strain C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 *sequence_revision 14-Dec-2001 *text_change 11-Jan-2002
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                                                                                                                                   A; Cross-references: GB:BA000019; FA; Experimental source: strain PCC
                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-251 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X81584; NID:g550386; PIDN:CAA57274.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-238 <RES>
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                                                                                                                                                                                                                        A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A, Title: The genome sequence of the facultative intracellular pathogen Brucella melit A; Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A;Reference number: AB0502; PMID:11677608

A;Accession: AE0940
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A; Residues: 1-254 < PAR>
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probable zinc-finger protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_chang
C;Accession: A84682
                                                                                                                                                                                                                                                                                                                           A;Gene: BMEII0506
A;Map position: II
C;Superfamily: oligopeptide permease protein oppB
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A;Residues: 1-276 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL53748.1; PID:g17984674; GSPDB:GN00191
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R:LLD, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Toom, C.D.; Fujii, C.Y.; M.; Koo, H.; Mofat, K.S.; Conlin, L.A.; Shen, M.; Vanoken, S.E.; Umayam, L.; Tillon, L. Reuss, D.; Nierman, M.C.; Mhite, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A. Residene Googlember and analysis of chromosome 2 of the plant Arabidopsis thaliana. A.; Satus: Fraser Benedics: DRA 62002093; MJD.20083489

A.; Satus: Fraser Benedics: GRACO2093; MJD.94803561; FIDM:AAD29833.1; GSPDB:GN00139
A.; Residues: 1-284 STD.
A.; Came: A.223200
A.; Gene: A.223200
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p52828 pseudomonas
p47880 mus musculu
p70796 agrobacteri
        P36549
Q99165
Q9kjv3
Q9cj03
Q9cad9
Q9va1
Q9wva1
P56380
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P56498
Q60288
P06774
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P48785
O76819
Q9szw4
P45596
Q9wxk8
P24366
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P48760
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P38748
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P55225;
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"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";

Nature 413:848-852(2001).
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SPECIES=S.enteritidis; STRAIN=27655-3B; MEDLINE=96146512; PubMed-8550497; Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., "Salmonella enteritidis agfBAC operon encoding thin, aggr
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01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Major curlin subunit precursor (Fimbrin SEF17).
CSGA OR AGFA OR STM1144 OR STY1181.
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Grewal N., Mulvaney E.,
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.A., Kay W.W.
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MEDLINE-94013373; PubMed-8104955;
Doran J.L., Collinson S.K., Burian J., Sarlos G., T
Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., F
MUNRO C.K., Kay C.M., Banser P.A., Peterkin P.I., F
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Oshima T., Aiba H., Baba T., Fuj
Ikemoto K., Inada T., Itoh T., K
Kinura S., Kitagawa M., Makino K
Mori H., Motomura K., Nakamura Y
Sampei G., Seki Y., Tagami H., T
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-K12 / MC4100;
MEDLINE-96414468; PubMed-8817489;
Hammar M., Arnqvist A., Bian Z., Olsen A., Normark S.;
"Expression of two csg operons is required for product "Expression of two csg operons is required for product "Expression of two csg operons is required."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The RpoS sigma factor relieves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=K12 / W3110;
                                           use by
modified
                                                                                                                                                                                                                                                                                                                   MEDLINE-930/23873; PubMed=1357528; Arnqvist A., Olsen A., Pfeifer J., "The Crl protein activates cryptic fibronectin binding in Escherichia Mol. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                             Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repression of csgA, Escherichia coli.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                            MEDLINE=91310586; PubMed=1677357; Collinson S.K., Emoedy L., Trust T.J., Kay Furification and characterization of thin, salmonella enteritidis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science
                                                                                                                                                                          SEQUENCE OF 21-40.
STRAIN-K12 / YMEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                      This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97061202;
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SIMILARITY:
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                                                                                                                                                           FIBRONECTIN
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                                                                                                                                STRONG,
TO CURL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Baba T., Fujita K., Hayashi K., Honjo A.,
r., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
a M., Makino K., Masuda S., Miki T., Mizobuchi K.,
r., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Tagami H., Takemoto K., Wada C., Yamamoto Y.,
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CURLIN MINOR SUBUNIT (CSGB).
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gene of fibronectin-binding c
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                                                                                                                                                                                                                                                                                                                                      Russell D.G., Normark S.; genes for curli formation coli HB101.";
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on the linkage map.";
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Best Local
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Q9X6E8;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blumer C., Heeb S., Pessi G., Haas D.;

"Global GacA-steered control of secondary metabolism in Pseudomonas fluorescens acts on specific ribosome binding sites.";

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: THIS PROTEIN BINDS DIRECTICY TO 23S RIBOSOMAL RNA AND IS NECESSARY TO THE IN VITRO ASSEMBLY PROCESS OF THE 50S RIBOSOMAL SUBUNIT; IT IS NOT INVOLVED IN THE PROTEIN SYNTHESIZING FUNCTIONS OF THAT SUBUNIT (BY SIMILARITY).

OF THAT SUBUNIT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                               EMBL; AF136400; AAD34789.1; -.
InterPro; IPR001081; Ribosomal_L20.
Pfam; PF00453; Ribosomal_L20; 1.
                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EcoGene; EG11489; CsgA.
EcoGene; EG11489; CsgA.
Fimbria; Signal; Complete proteome.
STGNAL 1 20
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                                                                                                                                                                                                       PRINTS: PRO0062; RIBOSOMALL20.
PRODOM: PD002389; RIBOSOMALL20: 1.
PROSITE: PS00937; RIBOSOMALL20: 1.
RIBOSOMAL L20: 1.
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16-OCT-2001
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104
                                                                                        Local Similarity
nes 7; Conserv
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L; X90754; CAA62282.1; -. 

L; AE000205; AAC74126.1; -. 

L; D90741; BAA35832.1; -. 

L; D90742; BAA35840.1; -. 

C70742; BAA35840.1; -. 

C707
AAFAAIV 110
                   AAFAAIV 13
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                                                                                                                                                                                     118 AA;
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(Rel. 39, Last seq
(Rel. 40, Last ann
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n L20.
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                                                                                      Score 7; DB 1; Pred. No. 7.8
0; Mismatches
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A -> E (IN REF. 1).
; C003470D208D395F CRC64;
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Pred. No. 0.00095;
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                                                                                                            DB 1;
5. 7.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
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                                                                                                                                    Length 118;
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                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Suppression of a sensor kinase-dependent phenotype in Pseudomonas syringae by ribosomal proteins 135 and 120.";
J. Bacteriol. 178:1548-1555(1996).
-i- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND NECESSARY TO THE IN VITRO ASSEMBLY PROCESS OF THE 50S RIBOSOMAL SUBUNIT; IT IS NOT INVOLVED IN THE PROTEIN SYNTHESIZING FUNCTIC OF THAT SUBUNIT (BY SIMILARITY).
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P52828;
                                                                                                                                P47880;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update
Insulin-like growth factor binding protein (IBP-6) (IGP-binding protein 6).
IGFBP-6 OR IGFBP-6.
                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00062; RIBOSOMALL20.

PRODOM; PD002389; Ribosomal_L20; 1.

PROSITE; PS00937; RIBOSOMAL_L20; 1.

Ribosomal protein; rRWA-binding.

SEQUENCE 118 AA; 13314 MW; 2BF171F5681EE443 CRC64;
MEDLINE-95121750; PubMed-7529732; Schuller A.G.P., Groffen C., van Drop S.L.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996
16-OCT-2001
                                        TISSUE=Liver;
                                                                                            Mammalia; Eutheria;
                                                                                                         Eukaryota; Metazoa;
                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001081; Ribosomal_L20
Pfam; PF00453; Ribosomal_L20; 1.
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                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U44118; AAB05016.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas syringae (pv.
                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                IBP6_
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                                                                                                                                                                                                                                                                                                                       7 AAFAAIV 13
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6 (Rel. 34, Last sequ
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mal protein L20.
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                                                                                            Chordata;
Rodentia;
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               van Neck J.W.,
                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                 Pred. No. 7. 
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Hypothetical 31.6 kDa protein in
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SMART; SM00211; TY;
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InterPro; IPR000716; Thyroglobulin_1.
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                             MEDLINE=96252899;
                                                                                     SEQUENCE FROM N.
                                                                                                                                      NCBI_TaxID=373;
                                                                                                                                                              Bacteria; Proteobacteria;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                            Plasmid
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PROSITE; PS00484; THYROGLOBULIN_1; 1.
Growth factor binding; Signal; Glycoprotein.
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SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
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PF00086; thyroglobulin_1; 1.
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              Federspiel N., Hyman R., Kalman S.
Namath A., Oefner P., Roberta P.
Submitted (NOV-1006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHPB_ECOLI STANDARD; PRT; 314 AA. PS471; P77461; P77048; O1-OCT-1996 (Rel. 34, Created) O1-NOV-1997 (Rel. 35, Last sequence update) O1-NAR-2002 (Rel. 41, Last annotation update) Z,3-dihydroxyphenylpropionate 1,2-dioxygenase MHPB OR B0348 OR Z0446 OR ECS0403.
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modified and this statement is not removed.
entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                      STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
MEDLINE-97426617; pubmed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-K12 / CS520; Ferrandez A., Garci
                                                                                                                                                                                                                                                                                                             Spence E.L., Kawamukai M., Sanvoisin J., Braven H., "Catechol dioxygenases from Escherichia coli (MhpB) eutrophus (MpcI): sequence analysis and biochemical third family of extradiol dioxygenases.";
J. Bacteriol. 178:5249-5256(1996).
                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12 / W3110;
MEDLINE=96359381; PubMed=8752345;
Spence E.L., Kawamukai M., Sanvol
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Mau B., Shao Y.;
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                                     Aparicio A.M., Chung E., S., Komp C., Kurdi O., Le ., Schramm S., Davis R.W.;
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Repeat; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyam Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T. Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli" O157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D86239; BAA13053.1; -. EMBL; Y09555; CAA70748.1; -. EMBL; AE000142; AAC73451.1; -.
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MEDLINE-21156231; PubMed-11258796;
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MEDLINE=21074935; PubMed
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01-NOV-1995
16-OCT-2001
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NP_BIND 19 26 GTP (BY SIMILARITY).
NP_BIND 81 85 GTP (BY SIMILARITY).
NP_BIND 136 139 GTP (BY SIMILARITY).
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InterPro; IPR004161; GTP_EFTU_D2.
InterPro; IPR004160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU, 1.
Pfam; PF03144; GTP_EFTU_D2; 1.
Pfam; PF03143; GTP_EFTU_D3; 1.
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-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94368062; PubMed=8085791;
Ludwig W., Neumaler J., Klugbauer N., Brockmann E., Roller C.
Klugbauer S., Reetz K., Schachtner I., Ludvigsen A.,
Bachleitner M., Fischer U., Schleifer K.H.;
"Phylogenetic relationships of Bacteria based on comparative
Chloroplast.
Eukaryota; Viridiplantae;
NCBI_TaxID=13779;
                                  Chara connivens.
                                                                                                                                    CHACO
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Bacteria; CFB group;
NCBI_TaxID=979;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
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SUBCELULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BIN
EF-TU/EF-1A SUBFAMILY.
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           Streptophyta; Characeae;
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InterPro: IPRO04161; GTP_EFTU_D2.
InterPro: IPRO04160; GTP_EFTU_D3.
Pfam; PF00009; GTP_EFTU_D2: 1.
Pfam; PF03144; GTP_EFTU_D2: 1.
Pfam; PF03144; GTP_EFTU_D3: 1.
Pfam; PF03143; GTP_EFTU_D3: 1.
PRINTS; PR00315; ELONGATNECT.
PROSITE; PS00301; EFACTOR_GTP; 1.
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SEQUENCE FROM N.A.
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MEDLINE-95392822; PubMed-7663757;
Delwiche C.F., Kuhsel M., Palmer J.D.;
Phylogenetic analysis of tufA sequences indicates a cyanobact origin of all plastids.";
Mol. Phylogenet. Evol. 4:110-128(1995).
HOLOGENET THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      YHBO_YEAST
P38748;
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                                      Johnston M., Andrews S., Brinkman R., Cooper J., Ding H.,
Johnston M., Andrews S., Brinkman R., Geisel C., Kirst
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirst
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Kucaba T., Hillier L., Jier M., Macric C., Mardis E., Menezes S.,
Latreille P., Louis E.J., Macric C., Mardis E., Wenezes S.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., V
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson F
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Mendel; 13588; CHAco; TufA; 1
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MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical YHL010C.
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Saccharomycetales; Saccharomyc
     Vaudin M.;
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SUBCELLULAR LOCATION: (
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                 Saccharomycotina;
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                                                                                                                                                                                                                                                                                                                                                                                                                      intergenic
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                                                                                                                                                 C., Kirsten
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sten J.,
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RESULT 11
FOLC_HUMAN
FOLC_HUMAN
IDC_G059;
AC Q059;
DT 01-Q0
DT 01-Q0
DT 01-Q0
DT 6019;
GN FPGS
RM GDLL
RN GAT
RN FISS
RX MEDLL
RN [3]
RP FTGE
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Best Local S
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SGD; S0001002; YHL010C.

InterPro; IPR001841; Znf_Ting.

InterPro; IPR001607; Zf-UBP.

Pfam; PF00097; Zf-C3HC4; 1.

Pfam; PF002148; Zf-UBP; 1.

SMART; SM00284; RING; 1.

SMART; SM00290; ZnF_UBP; 1.

PROSITE; PS00518; ZF_RING_1; F,

PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; ZN_FING 240 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U11582; CAB34905.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Folylpolyglutamate synthase, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FOLC_HUMAN Q05932;
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Proc. Na
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Freemantle S.J., Taylor S.M., Krystal G., Moran R.C "Upstream organization of and multiple transcripts folylpoly-gamma-glutamate synthetase gene.";
J. Biol. Chem. 270:9579-9584(1995).
                                                                                                                                                                                                                                                  Garrow T.A., Admon A., Shane B.;
"Expression cloning of a human cDNA encoding
                                                                                                                                                                                                                                                                                               TISSUE=Lymphocytes;
MEDLINE=93028422; PubMed=1409616;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 20-587
                                                                                                                                                                                                                                                                                                                                                                                       Submitted
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                                                                                     MEDLINE=95238480; PubMed=7721888;
                                                                                                                                                                                                         folylpoly(gamma-glutamate) synthetase and determination
primary structure.";
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                                                                                                                 rissue-Placenta.
                                                                                                                                       SEQUENCE
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Qi H., Korenberg J.
d (JUL-1995) to the
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Pred. No.
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RESULT 12
FOLC_MOUSE
ID FOLC_MOUSE
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                                                                                                                                          Query Match
Best Local
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EMBL; U40863; AAA87568.1; J
EMBL; U40864; AAA87568.1; J
EMBL; U40865; AAA87568.1; J
EMBL; U40865; AAA87568.1; J
EMBL; U40867; AAA87568.1; J
EMBL; U40867; AAA87568.1; J
EMBL; U40867; AAA87568.1; J
EMBL; U24253; AAC13871.1; EMBL; U24253; AAC13871.1; J
PTR; A46281; A46281.
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Clhowler D.J., Shane B.;

"Mammalian folylpoly-gamma-glutamate synthetase. 1. Purification

"general properties of the hog liver enzyme.";

Blochemistry 26:504-512(1987).

-I- FUNCTION: CONVERSION OF FOLATES TO POLYGLUTAMATE DERIVATIVES.

ALLOWS TISSUES TO CONCENTRATE FOLATE AT HIGHER LEVELS THAN IN
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NP_BIND
CONFLICT
SEQUENCE
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EMBL;
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                                                                                                                                                                                                                                                                    PROSITE; PS01011; FOLYLPOLYGLU_SYNT_1; 1.
PROSITE; PS01012; FOLYLPOLYGLU_SYNT_2; 1.
Ligase; One-carbon metabolism; ATP-binding; Mitochondrion;
Transit peptide; Alternative initiation.
                                                                                                                                                                                                                                                                                                                            InterPro; IPR001645; FOLYLPOLYGLU_SYNT
InterPro; IPR004101; Mur_ligase_C.
Pfam; PF02875; Mur_ligase_C; 1.
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MIM; 136510; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetase gene: evidence for a Cancer Res. 55:6030-6034(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taylor S.M., Freemantle S.J., Moran R.G.;
"Structural organization of the human folypoly-gamma-glutamate
synthetase gene: evidence for a single genomic locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96105015; PubMed-8521387;
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SEQUENCE OF 102-587 FROM
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                                                                                                 54 NAALALQ
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by non-profit institutions as long as its content
ified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORM
BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FF
SIMILARITY: BELONGS TO THE FOLYLPOLYGLUTAMATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: MONOMER
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                                                                        NAALALQ
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                                                                                                                             Similarity
7; Conserv
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    STANDARD;
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TO OUTOPLASMIC ISOFORM.
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Pred. No.
    PRT;
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J. Biol. Chem. 270:26918-26922(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P48760;
01-FEB-1996 (Rel. 33, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Folylpolyglutamate synthase, mitochondrial pr
                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: ATP + {tetrahydrofoly1-[Glu]}(N) + L-glutal = ADP + phosphate + {tetrahydrofoly1-[Glu]}(N+1).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Mitochondrial and cytoplasmic.
-!- ALTERNATIVE PRODUCTS: A SINGLE NUCLEAR GENE PRODUCES BOTH FORM.
BY USE OF ALTERNATIVE INITIATION CODONS IN THE SAME READING FR.
-!- SIMILARITY: BELONGS TO THE FOLYLPOLYGLUTAMATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spinella M.J., Brigle K.E., Goldman I.D.;
"Molecular cloning of murine folylpoly-gamma-glutamate synthetase.";
Biochim. Biophys. Acta 1355:11-14 (1996)
-i- FUNCTION: CONVERSION OF FOLATES TO POLYGLUTAMATE DERIVATIVES. TH
                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                   SEQUENCE
                                                                                                                                                                                   TRANSIT
                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                  PROSITE; PS01011;
                                                                                                                                                                                                                                             Pfam; PF01225; Mur_ligase;
                                                                                                                                                                                                                                                           MGD; MGI:95576; Fpgs.
InterPro; IPR001645; FOLYLPOLYGLU_SYNT
                                                                                                                                                                                                                                                                                                 EMBL; U33557; AAC52812.1;
EMBL; U32197; AAC52426.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96180977; PubMed=8605241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=DBA/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Mammalia; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                           Ligase;
                                                                                                                                                                                                                                                                                        HSSP; P15925; 1FGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96070787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Folylpoly-gamma-glutamate synthetase) (FPGS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALLOWS TISSUES TO CONCENTRATE FOLATE AT HIGHER LEVELS
 Similarity
7; Conser
                                                                                                                                                                                            peptide;
                                                                                                                                                                                                      PS01012; FOLYLPOLYGLU_SYNT_2: 1.
One-carbon metabolism; ATP-binding; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Metazoa; Chordata;
Eutheria; Rodentia;
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43
103
103
27
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35
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138
491
491
 Conservative
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                                                                                                                                                                                              Alternative
                                                                                                                                                                                                                        FOLYLPOLYGLU_SYNT_1; 1. FOLYLPOLYGLU_SYNT_2; 1.
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109
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                                                   64907
             4.6%;
100.0%;
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                                                           FOLYLPOLYGLUTAMATE SYNTHA
FOR CYTOPLASMIC ISOFORM.
ATP (POTENTIAL).
P -> A (IN REF. 2).
G -> W (IN REF. 2).
QL -> HV (IN REF. 2).
R -> S (IN REF. 2).
D -> E (IN REF. 2).
 0;
             Score 7;
                                                                                                                                                                                              initiation
                                                                                                                                                                                  MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                   B43FB8915EB64E05
 Mismatches
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0;
                       Length 587;
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Indels
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; Murinae; Mus
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Best Local
    PRH_ARATH
P48785;
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Q9WTV7;
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ZN_FING
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00184; RING; 1.
PROSITE; PS00518; ZF_RING_1; FALSE_NEG PROSITE; PS50089; ZF_RING_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00097; zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1342291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institumodified and this statement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Opposing developmental functions of positive and negat: coregulators of LIM homeodomain factors."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99364422; PubMed=10431247;
Bach I., Rodriguez-Esteban C., Carriere C.,
Rose D., Glass C.K., Andersen B., Izpisua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bach
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001
                                                                                                                                                                                                                       34 GGGNSSG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX FACTORS. SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CT-2001 (Rel. 40, Last sequence update)
CT-2001 (Rel. 40, Last annotation update)
finger protein 12 (LIM domain interacting RING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s requires a license agreement (Some mail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
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IPR001841; Znf_ring.
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415 484
546 587
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                                                           STANDARD;
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SER-RICH.
                                                                                                                                                                                                                                                                Score 7; DB 1; Pred. No. 32; 0; Mismatches
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RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Ramborth S., Koetter P., Ramodijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R., RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S., RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S., RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S., RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S., Ray M., Lennard N., McLay K., Mayes R., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., RA Clark L., Doggett J., Fartmann B., Granderath K., Dauner D., Herzl A., Ray Dose S., de Haan M., Marse A.C., Schaefer M., Mueller-Auer S., RA Bockova D., Bloecker H., Scharfe M., Granderath K., Dauner D., Herzl A., RA Massenet O., Ouigley F., Clabauld G., Muendlein A., Felber R., RA Massenet O., Ouigley F., Clabauld G., Muendlein A., Felber R., RA Massenet O., Ouigley F., Clabauld G., Muendlein A., Felber R., RA Chafdor F., Cooke R., Berger C., Monfort A., Casacuberta E., RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A., RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C., RA Frishman D., Haase D., Lencke K., Mewes H.-W., Stocker S., RA Ra Ratner D., Bevan M., Wilson R.K., de la Bastide M., Habermann K., RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L., RA Schon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., RA Atreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Hillier I...
Kramer J., Fulton L., Mardis E., Dante M., Greco T., Kemp K., Nelson J., Spieth J., Ryan E., Dante M., Pepin K., Hillier L., Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu Antonolu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah I. Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A. Chen E., Marra M., Martienssen R., McCombie W.R.;
"Sequence and analysis of chromosome 4 of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N., Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Melchselgartner M., de Simone V., Obermaier B., Mache R., Mueller M., Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., Reichert B., Porfetelle D., Perez-Alonso M., Boutry M., Bancroft I., Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., Braneken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
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16-0CT-2001 (Rel. 40, Last annotation update)
Pathogenesis-related homeodomain protein (PRHA).
PRH OR PRHA OR AT4G29940 OR F27B13.180.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheof Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plesch G., Stoermann K., Tovar To
"Developmental and auxin-induced
homeobox gene.";
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MEDLINE=98012533; PubMed=9351248;
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"Plant homeodomain protein involved in
a pathogen defense-related gene.",
Plant Cell 6:695-708(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. COLUMBIA;
MEDLINE=94312876; PubMed=7913642;
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                                                                                                                                                                        A., Shah R.,
                                                                                                                                                                                                          Joshu C.,
dan C.,
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Pfam; PF00046; homeobox; 1.
Pfam; PF000628; PHD; 1.
SMART; SM00389; HOX; 1.
SMART; SM00249; PHD; 1.
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DOMAIN
REPEAT
SEQUENCE FROM N.A.

Duportets L., Rossignol F., Couillaud F.;

"Molecular cloning and tissue expression of 3-hydroxy-3-methylglutaryl coenzyme A reductase of the black cutworm Agrotis ipsilon.";

Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                Agrotis ipsilon (Black cutworm moth).

Bukaryota; Metazoa; Arthropoda; Trachaeta; Hexapo Pterygota; Neoptera; Endopterygota; Lepidoptera; Noctuoidea; Noctuidae; Noctuinae; Agrotis.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-hydroxy-3-methylglutaryl-coenzyme A reductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L21991; AAA32843.1; -. U48864; AAC49836.1; -.
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CAPALYTIC ACTIVITY: (R)-mevalonate + CoA + hydroxy-3-methylglutaryl-CoA + 2 NADDH.
ENZYME REGULATION: THE ACTIVITY OF HMG-COA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE HMG-COA REDUCTASE FAMILY
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SGSALAG
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PS00066; HMG_COA_REDUCTASE_1;
PS00318; HMG_COA_REDUCTASE_2;
PS01192; HMG_COA_REDUCTASE_3;
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                                                                                                                   Similarity 7; Conserv
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   GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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                               033802 salmonella
054069 salmonella
09r4t8 salmonella
09r3j5 escherichia
09x3j5 escherichia
09xa68 streptomyce
09xa77 streptomyce
09xa77 streptomyce
09xa91 streptomyce
0911c0 streptomyce
0911c0 streptomyce
099160 staphylococ
09ae10 corynebacte
09colf pasteurella
          Q9aqd9 lactococcus
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 Q94an7 arabidopsis
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Best Local Similarity
Matches 127; Conserv
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SEQUENCE FROM N.A.
MEDLINE-98053981; PubMed-9393832;
SUKUPOIVI S.S., Lorentz R.G., Gordon J.I., Bian Z., Pfeifer J.D.,
Normark S.J., Rhen M.;
Normark S.J., Rhen M.;
"Expression of thin, aggregative fimbriae promotes interaction of
"Expression of thin, aggregative fimbriae promotes interaction of
"Expression of thin, aggregative fimbriae promotes interaction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O33802 PRELIMINARY;
O33802;
O1-JAN-1998 (TrEMBLrel. 05,
O1-JAN-1998 (TrEMBLrel. 05,
O1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Infect. Immun. 65:5320-5325(1997).

EMBL; AJ000514; CAA04151.1; -.

NON_TER 152 152

SEQUENCE 152 AA; 15401 MW; 9DA:
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Salmonella typhimurium.
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[1]
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    140 VGFGNNA 146
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                                                                                                                                                                                                                                                                               20 AGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGA 79
                                                                                                                           DVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQ 139
                                                                                                                                                                                                                                             AGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGA 79
                                                                                DVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQ 139
                                                                                                                                                                                                                                                                                                                                                                                             84.1%; Score 127; DB 2; Lot 100.0%; Pred. No. 5.5e-117; Conservative 0; Mismatches 0;
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Best Local Similarity
Thes 72; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                     Query Match
Best Local
                                                                        Stolpe H., Grund S., Schroder w.;
"Purification and partial characterization of type 3 fimbriae from Salmonella typhimurium var. copenhagen.";
Int. J. Med. Microbiol. Virol. Parasitol. Infect. Dis. 281:8-15(19: SEQUENCE 19 AA; 1910 MW; 9AD8B59D411E5B51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q54069;
Q54069;
Q1-NOV-1996
                                                                                                                                                                                                                     0984T8 PRELIMINARY; PRT; 19 AA.
0984T8 PRELIMINARY; PRT; 19 AA.
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Lastisequence update)
01-JUN-2000 (TrEMBLrel. 14, Lastisenotation update)
                                                                                                                                        MEDLINE=95102231; PubMed=7803933;
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                    Salmonella.
                                                                                                                                                                                            Bacteria; Proteobacteria;
                                                                                                                                                                                                      Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cox J.M., Eglezos S., Woolcock J.B.;
"Virulence of Salmonella enteritidis in chickens correlates
colony morphology and expression of SEF17 fimbriae.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-SE30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Salmonella.
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                                                                                                                                                                         NCBI_TaxID=602;
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                    21 GVVPQWGGGGNHN 33
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                                                     Similarity
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                                          Mismatches
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4e-63;
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RESULT 4

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  Q9XA68;
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01-NOV-1999
01-NOV-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=43895 RED VARIANT;
MEDLIIN=-21218556; PubMed=11319125;
Milch G.A., Keen J.E., Elder R.O.;
Multations in the csgD Promoter Associated with Variations 'Mutations in the csgD Promoter Associated with Variations Expression in Certain Strains of Escherichia coli O157:H7."
Expression in Certain Strains of Escherichia coli O157:H7."
Appl. Environ. Microbiol. 67:2367-2370(2001).
EMBL; AF275733; AAK53212.1; -.
EMBL; AF275733; AAK53212.1; -.
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Q9S3J5;
01-MAY-2000
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01-DEC-2001
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Non-curliation of Escherichia coli 078:K80 iso
ISI inserti on in csgB and reduced persistence
FEMS Microbiol. Lett. 175:247-253(1999).
EMBL; AJ131756; CAB45380.1;
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01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-MAR-2001 (TYEMBLrel. 16, Last annotation update)
CURLIN SUBUNIT MONOMER (FRAGMENT).
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Q9XAR7;
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Q1-NOV-1999
Q1-DEC-2001
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Bentley S.D.,
Submitted (JUN
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Submitted
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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; aset of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
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                                                                                                                           MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes;
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                                                                                                                                                                                           SEQUENCE FROM N.A.
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Kinashi H., Hopwood D.A.;
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1. Microbiol. 21:77-96(1996).
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C-2001 (TrEMBLrel. 1
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d (JUL-1999)
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                                                                                                                                                                                                                                                    .D., Parkhill J., 1 (JUN-1999) to the
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
DEHYDROGENASE SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill
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to the EMBL/GenBank/DDBJ databases
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the EMBL/GenBank/DDBJ databases
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e EMBL/GenBank/DDBJ databases.
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hromosome.";
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Matches
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01-NOV-1999 (TrEMBLrel. 12, Cres
01-NOV-1999 (TrEMBLrel. 12, Las
01-DEC-2001 (TrEMBLrel. 19, Las
HYPOTHETICAL 6.6 KDA PROTEIN.
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-: CATALYTIC ACTIVITY: NADH + UBIQUINONE =
-: CATALYTIC ACTIVITY: NADH + UBIQUINONE =
-:- SUBCELJULAR LOCATION: INTEGRAL MEMBRANE
EMBL; AL078618; CAB44518.1; -
InterPro: IPR001750; Oxidored_q1.
Pfam; PF00361; Oxidored_q1; 1.
NAD; Oxidoreductase; Transmembrane.
SEQUENCE 552 AA; 57362 MW; A74E40FEA914E
                                                          Q9L1CO;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinashi H., Hopwood D.A.;

"A set of ordered cosmids and a detailed genetic athe 8 Mb Streptomyces coelicolor A3(2) chromosome.

Mol. Microbiol. 21:77-96(1996).

EMBL; AL096837; CAB48911.1; -.
Streptomyces
                      PUTATIVE INTEGRAL MEMBRANE SCL11.18.
                                                                                                                                         Q9L1C0
                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein SEQUENCE 62 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       James K.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seeger K., Harris D.;
Submitted (JUL-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seeger K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97000351; PubMed=8843436;
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                                                                                                                                         PRELIMINARY;
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    coelicolor
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100.0%;
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the EMBL/GenBank/DDBJ databases
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Pred.
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Streptomyces.
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21;
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(BY SIMILARITY).
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Q9SDX8;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PHOSPHOENOLPYRUVATE CARBOXYLASE KINASE (FRAGMENT).
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                                               NON_TER
SEQUENCE
                                                                           InterPro; 1PKVV22....
pfam; PF00059; pkinase; 1.
pROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
pROSITE; PS00108; PROTEIN_KINASE_ST; 1.
pROSITE; PS00108; Provate; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A set of ordered cosmids and a detailed genetic and the 8 mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; AL157953; CAB76405.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                             Brassica napus (Rape)
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Brass;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97000351; PubMed=8843436;
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                                                                   Transferase.
                                                                                                                                                                                                                              MEDLINE=20040078; PubMed=10571893;
Hartwell J., Gill A., Nimmo G.A., Wilkins M.B.,
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               NCBI_TaxID=3708;
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                                                                                                                                                                                                           "Phosphoenolpyruvate carboxylase kinase
                                                                                                                                                                                                                         Nimmo H.G.;
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|||||||
54 SALAGVV 60
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Similarity 7; Conserv
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145 AA;
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 4.6%; ilarity 100.0%; Conservative
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EMBL/GenBank/DDBJ databases.
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  Score 7; DB 1; Pred. No. 64; 0; Mismatches
   0;
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                                                A90350EA032457F1 CRC64;
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              DB 10;
5. 64;
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   0,
                        Length 145;
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Q99U60
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MEDLINE-21311952; PubMed-11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain M150). Bacteria; Firmicutes; Bacillus/Clostridium groBacillus/Staphylococcus group; Staphylococcus. NCBI_TaxID=158879, 158878;
                                                                                                             wehmeler L., Schafer A., Burkovski
Malke H., Puhler A., Kalinowski J
"The role of the Corynebacterium g
metabolism.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9AE10;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HOLLIDAY JUNCTION DNA-HELICASE RUVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lancet 357:1225-1240(2001).
EMBL; AP003133; BAB42521.1;
EMBL; AP003362; BAB57590.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole genome aureus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; SEQUENCE 145 AA; 16
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=AFCC13032;
MEDLINE=98361031; PubMed=9695918;
                                                                                                                                                                                                                                                                                                                     Corynebacterium.
NCBI_TaxID=1718;
                    SEQUENCE FROM N.A. STRAIN=ATCC13032;
                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae;
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                                                                                                Microbiology
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Kalinowski
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Conservative
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                                                                                                  144:1853-1862(1998)
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16014 MW;
  J.,
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  Puhler
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245ECA4104A63875 CRC64
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Best Local
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"Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

EMBL; AE006167; AAK03364.1; -.

InterPro; IPR000056; Ribul_P_3_epim.

Pfam: PF00834; Ribul_P_3_epim; 1.

Complete proteome.

SEQUENCE 229 AA:
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01-JUN-2001
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01-JUN-2001
01-JUN-2001
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SEQUENCE
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                                                                                                                                                         RRB.
Lactococcus lactis.
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Pasteurella multocida.
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                                                                                                                                                                                                                                                                                                                                                                                                Q9AQD9
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InterPro; IPR000085; Ruva.
Pfam; PF01330; Ruva; 1.
                                                             NCBI_TaxID=1358;
                                                                                               Lactococcus
                                                                                                                             Bacteria; Firmicutes;
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7; Conservative
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(TremBLrel. 17, Last seq
(TremBLrel. 19, Last ann
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                                                                                                                          Bacillus/Clostridium group; Streptococcaceae;
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0; Mismatches
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O'Connell-Motherway M., van Sinderen D., Morel-
Fitzgerald G.F., Ehrlich S.D., Morel P.;
"Six putative two-component regulatory systems
Lactococcus lactis subsp. cremoris MG1363.";
                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactococcus lactis subsp. cremoris MG1363.";
Microbiology 146:935-947(2000).
-:- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
-:- SIMILARITY: TO OTHER BACTERIAL REGULATORY PROTEINS INVOLVED IN
                                                                                                                                        SEQUENCE
                                                                                                                                                  Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC012723; AAH12723.1; -.
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Mammalia; Eutheria;
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Interpro; IPR001867; Trans_re
Pfam; PF00072; response_reg;
Pfam; PF00486; trans_reg_C; ]
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA (segmence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native back into the chromosome of the homologous species, replacing the native
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                                                                                                                                                              Disclosure; Page 135; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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RESULT 3
AAW23570
ID AAW2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qγ
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QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AgfA protein containing a replacement segment or segments of foreign CC amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and cinexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                           29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW23570 standard; Protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                     Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis 27655-3b agfA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW23570;
           enteropathogenic bacteria of the
                        Isolated Salmonella gene agfA - used for diagnosis of Salmonella
                                                                                                                                                  26-APR-1994;
26-APR-1993;
                                                                                                                                                                                         26-APR-1993;
                                                                                                                                                                                                                   03-JUN-1997
                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis
                                                                                                                     (UYVI-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLLKYAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                    1997-309886/28.
DB; AAT74142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNAALVNOTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                             SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                        VICTORIA INNOVATION & DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                             Collinson
                                                                                                                                                  94US-0233788
93US-0054452
                                                                                                                                                                                         93US-0054452
                                                                                                                                                                                                                                                                                     Location/Qualifiers 123
                                                                                                                                                                                                                                                                       /note= "Encoded by GCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.0%;
                                                                                             SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 773; DB 21;
Pred. No. 1.8e-65;
Mismatches 0;
                                                                                             Doran
              Enterobacteria
                                                                                             JL,
                                                                                                                         CORP
                                                                                             Kay WW
               family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Example 2; Fig

7;

85pp; English

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ARBSOLT 4
AABJA AABJA
AABJA AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents agfA encoded by the full agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 9% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from the provide animals relative to nucleic acid molecules from the provided animals relative to nucleic acid molecules from the provided animals relative to nucleic acid molecules from the provided animals relative to nucleic acid molecules from the provided animals relative to nucleic acid molecules from the provided animals relative to nucleic acid molecules from the provided animals relative to nucleic acid molecules from the provided animals relative to nucleic acid molecules from the provided animals relative to nucleic acid molecules from the provided animals relative to nucleic acid molecules from the provided animals relative to nucleic acid molecules from the provided animals relative to nucleic acid molecules from the provided animals relative to nucleic acid molecules acid molecul
The present invention describes a recombinant agfA gene segment of the gene has been replaced by a segment of a
                                                                                                                              Disclosure;
                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-672631/65.
N-PSDB; AAC64622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-2000; 2000WO-CA00356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AgfA::PT3#1 amino acid sequence SEQ ID NO:12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB36346 standard; Protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virtually all other microbial organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNPALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Doran JL,
                                                                                                                         Page 135; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 5.3e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                               response in animal
(I) where a foreign DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc sequence which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended

cc assembly system of strains of Salmonella, Escherichia coli and

cc Enterobacteriaceae for the production of fimbriae comprising recombinant

cc AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively: (2)

cc directing recombination of a recombinant gene into the chromosome of the

cc homologous species; (3) directing recombination of a recombinant

cc back into the chromosome of the homologous species, replacing the native

cc copy of that gene; and (4) eliciting an immune response in an animal,

cc comprising separating an amino acid polymer comprising a recombinant

cc AgfA protein containing a replacement segment or segments of foreign

cc amino acid sequence or sequences grown on a Salmonella, E. coli or

cc Enterobacteriaceae host cell, from the host cell and introducing the

cc useful for the expression of recombinant AgfA protein which is useful

cc useful for the expression of recombinant AgfA protein which is useful

cc useful for the expression of recombinant AgfA protein which is useful

cc of eliciting an immune response in an animal. In a fimbrial presentation

cc system the heterologous antigens are presented in high numbers (up to

cc immunogenicity and adhesion properties relevant for an efficient live

cu condition the carrier fimbrial subunit proteins are usually strong

cc immunogens, which may be important for directing an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                    Escherichia Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                    White AP,
                                                                                                                                    05-APR-2000; 2000WO-CA00356.
                                                                                                                                                                                                                 WO200060102-A2
                                                                                                                                                                                                                                                                                            Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                   vaccine;
                                                                                                                                                                                                                                                                                                                                                 Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#2 amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                              26-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB36347 standard; Protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                        (UYVI-) UNIV VICTORIA.
                                                                                                                                                                          12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \vdash
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAFAAIVVSGSALAGVVDQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNAALVNYDQLVTRVVTHEMAHANNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                 immune response;
                  Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 AA;
                                                                                                                                                                                                                                                                          coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                               99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.9%;
90.1%;
                  Collison SK,
                                                                                                                                                                                                                                                                                                                                   immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 695; DB 21;
Pred. No. 4.2e-58;
                                                                                                                                                                                                                                                                                                                                                                                          NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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2000-672631/65

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RESULT 6
AAB36353
ID AAB3
XX AAB3
AC AAB3
XX AAB3
XX AAB3
XX SAB1
DT 26-F
XX Agfa
XX Salm
KW Vacc
XX Salm
OS Salm
OS Salm
OS Salm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC directing recombination of a recombinant gene into the chromosome of the CC back into the chromosome of the homologous species; (3) directing recombination of a recombinant gene CC back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant CC amino acid sequence or sequences grown or a Salmonella, E. coli or CC enterobacteriaceae host cell, from the host cell and introducing the CC useful for the expression of recombinant AgfA protein which is useful CC useful for the expression of recombinant AgfA protein which is useful CC system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response capainst the inserted epitope, and hybrid fimbriae are easy and consequence of the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                          Дb
                                                                                                                                                                                                                                                                                                                                                                                           δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                   Synthetic
                                                                                                              Salmonella;
                                                                                                                                                 AgfA::PT3#8
                                                                                                                                                                                                                                                                AAB36353 standard;
                                        Escherichia coli
                                                          Salmonella enteritidis
                                                                                             vaccine;
                                                                                                                                                                                        26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                           LVTRVVTHEMAHASVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITOSGYGNGADVGOGADNSTIELTQNGFRNNATIDOWNAKNSDITVGOYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bal Similarity
137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYDQ 120
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                                                                                               immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 AA;
                                                                                                                                                   amino acid sequence SEQ ID NO:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                              agfA; chromosomal
                                                                                                                                                                                        (first entry)
                                                                                               response;
                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.7%;
90.7%;
                                                                                                 1mmunogen
                                                                                                                                                                                                                                                                    151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 693; DB 21;
Pred. No. 6.5e-58;
3; Mismatches 11;
                                                                                                                gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                    Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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RESULT 7 AAB36349 ID AAB3

AAB36349 standard; Protein; 151 AA

AAB36349

В Ωy

121

NNAALVNQTASDSSVMVRQVGFGNNATANQY

151

120 120 60 60 Gaps

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В
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                                                                                                                                                                            QУ
                                                                                                                                                                                                                                                                                                                                                        comprising separating an amino acid polymer comprising a recombinant of AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coll or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful conjunction with a carrier or diluent. (I) is system the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live immunogens, the carrier fimbrial subunit proteins are usually strong cagainst the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombination of the chromosome of the homologous species; (3) directing recombination of a recombination of the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separation and manimal and comprising a proceedings.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-672631/65.
N-PSDB; AAC64629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 138; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                             the exemplification
121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                           61
                                                                                                 61
                                                                                                                                          \vdash
                                                                                                                                        MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALYDQ
                                                                                                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
                                                                              SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                       LVTRVVTHEMAHAGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                                                                                            similarity
                                                                                                                                                                                                                                                                                                       151 AA;
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                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0127888
                                                                                                                                                                                                                                                                                                                                                of the present invention.
                                                                                                                                                                                                                                              89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collison
                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                Score 692; DB 21;
Pred. No. 8.1e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SK,
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kay WW;
                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                 Length 151;
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26-FEB-2001

(first entry)

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Query Match
Best Local
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid sequence or sequences grown on Salmonella, E. coll or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign
                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enteritidis
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYVI-) UNIV VICTORIA
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                                       61
                                                                                                           Н
                                                                                                                                                                    1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                    AAC64625
                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                    151
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                                                                                                                                                                                                                                                                                                                                                                                 AA;
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                                                                                                                                                                                                                                                                            89.48;
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                                                                                                                                                                                                                                                                            Score 691; DB 2
Pred. No. 1e-57;
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay WW
                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                             Length 151;
                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                     Gaps
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В
                                                                                                                                                                                                                                                                                                     sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/RAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                        comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on Salmonella, E coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. [1]
                                  immunogens, which may be important for directing an immune res against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is
                                                                                                                                             useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to non conference).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB36352;
                                                                                         500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAC64628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White AP, Doran JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                    exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNAALVNQTASDSSVMVRQVGFGNNATANQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid sequence SEQ ID NO:24.
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RESULT 9
AAB36350
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Best Local
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                                                       assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant Agfa, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                                                          WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; immune response;
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comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the
                                                                                                                                                                                                                                                                                                                                                                                                                  (UYVI-) UNIV VICTORIA
                                                                                                                                                            The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
                                                                                                                                                                                                                                    Disclosure; Page 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosomal gene replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid sequence SEQ ID NO:20
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Pred. No. 1.2e-57
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RESULT 10
AAB36354
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                                                                                                                                        WPI; 200
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                                                                                    Recombinant agfA gene having a segment replaced by a foreign sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response
                                                                                                                                                                                                                                                                                                                                                             Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella;
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                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                  Escherichia
                                                                                                                                                                                                                                                                                                                                                                                        vaccine;
                                                   Disclosure;
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137; Conser
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                                                                                                                                          AAC64630
                                                                                                                                                                                                                                                                                                                                                                                        immune response;
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                                                                                                                                                                               Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                    agfA; chromosomal gene replacement;
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                                                                                                                                                                                                                                                                                                                                                  coli.
                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid sequence SEQ ID
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90.7%;
                                                 139pp; English.
                                                                                                                                                                                  Collison SK,
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Pred. No. 1.6e-57;
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The present invention describes a recombinant agfA gene (I) where segment of the gene has been replaced by a segment of a foreign D segmence which encodes a foreign epitope or antigen. Also describe

DNA

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RESULT 11
AAB36351
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WPI; 2000-672631/65
                                                              White AP,
                                                                                                                                                                                                         05-APR-1999;
                                                                                                                                                                                                                                                                       05-APR-2000; 2000WO-CA00356
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                                                                                                                                   (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; immune response; immunogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDARKSETTITQSGYGNGADYDQLVTRVVTHEMAHAFRNNATIDQWNAKNSDITVGQYGG
                                                              Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                         99US-0127888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.4%;
90.1%;
                                                                 Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 683; DB 21;
Pred. No. 5.7e-57;
1; Mismatches 14;
                                                                 Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Query Match

Length 151;

Sequence

151 AA;

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В

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В

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The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC Enterobacteriaceae for the production of finbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively: (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of a recombinant gene into the chromosome of the back into the chromosome of the homologous species; (4) eliciting an immune response in an animal, compyrising separating an amino acid polymer comprising a recombinant CC comprising separating an amino acid polymer comprising a recombinant CC comprising separating an amino acid polymer comprising a recombinant CC amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the CC useful for the expression of recombinant AgfA protein which is useful CC useful for the expression of recombinant AgfA protein which is useful CC immunogenicity and adhesion properties relevant for an efficient live craccine, the carrier fibrial subunit protein sore usually strong commonders, which may be important for directing a name response commonders.
                                                                         immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAC64627
                                                 exemplification of the present invention.
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δÃ δÃ В DЬ δÃ Best Local Similarity Matches 137; Conserv 121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151 61 61 SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120 ۲ 1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60 SDARKSETTITOSGYGNGADVGQGADNYDQLVTRVVTHEMAHADQWNAKNSDITVGQYGG Conservative 88.2%; 90.7%; 2; Score 682; DB 21; Pred. No. 7.1e-57; Mismatches Indels 0 Gaps 120 0

В

121 NNAALVNQTASDSSVMVRQVGFGNNATANQY 151

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RESULT 12
AAB36355
Salmonella enteritidis
                                                             Salmonella; agfA;
                                                                                                  26-FEB-2001
                                                                                                                                      AAB36355 standard; Protein; 151
                          Escherichia coli.
                                                                               AgfA::PT3#10 amino acid sequence SEQ ID NO:30
                                                     immune
                                                                                                 (first entry)
                                                   response;
                                                             chromosomal gene replacement; fimbrin; epitope;
                                                     immunogen
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WO200060102-A2

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Дb
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                         AAB36348
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                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a recombinant agfa gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA seguence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant Enterobacteriaceae for the production of fimbriae comprising value (2) finding the control of the cont
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AAB36348 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising separating an amino acid polymer comprising a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 139; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYVI-) UNIV VICTORIA
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                                                                                                                                                      121
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                                                                                                                                                                                                                                                                            61
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mes 137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of the present invention.
                                                                                                                                                                                                                                                                      MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                   NNAALVNQTASDSSVMVRQVGFGNNATANQV 151
                                                                                                                                                      NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                      MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
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   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.1%;
90.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collison SK,
   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 681; DB 21;
Pred. No. 8.9e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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61 61

SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG SDARKSETTITOSGYGNGADVGOGADNSTIELTONGFRNNATIDOWNAKNSDITVGOVGG

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                                                                                                                                                                                           back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal. Comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inserted epitope, and hybrid fimbriae are easy and the exemplification of the present invention.
                                                                             Query Match
Best Local S
Matches 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAC64624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaccine; immune response; immunogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AgfA::PT3#3 amino acid sequence SEQ ID NO:16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYVI-) UNIV VICTORIA
                           MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ
MKLLKVAAFAAIVVSGSALAGVYDQLVTRVVTHEMAHASGPDSTLSIYQYGSANAALALQ
                                                                                                Similarity
                                                                                                                                                             151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agfA; chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0127888
                                                                                                                                                             AA;
                                                                                                  85.1%;
90.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collison SK,
                                                                             Score 658; DB 21;
Pred. No. 1.3e-54;
3; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene replacement; fimbrin; epitope
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                                                                                                                     Length 151;
                                                                                  0;
                                                                                  Gaps
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ARESULT 14
AAR62761
ID AAR62
XX AAR62
XX AAR62
XX 26-JU
XX Salmc
XX Salmc
XX Salmc
XX Salmc
XX I0-W
YF 26-AI
YX (UYV)
XX WPI;
DR WPI;
CC The;
CC The;
CC The;
CC Salm
XX Sequ
                                                                                                         RESULT 15
AAW23569
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                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                      TophoA mutant strain AgfA protein. The encoding DNA and isolated AgfA protein are used in genetic immunization and vaccine compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-358275/44.
N-PSDB; AAQ73066.
           Salmonella enteritidis 27655-3b TnphoA mutant
                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents the Salmonella enteritis 27655-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clouthler SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enteritis 27655-3b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella; AgfA; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AgfA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR62761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR62761 standard; Protein; 120 AA
                                       29-SEP-1997
                                                                 AAW23569;
                                                                                           AAW23569 standard; Protein; 120 AA
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig7A; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KING/) KING J. (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-NOV-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 76.1%; So
Local Similarity 100.0%; I
nes 112; Conservative 0;
                                                                                                                                                               61
                                                                                                                                                                                         82
                                                                                                                                                                                                                                 22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                  1 VVPQWGGGGNHNGGGNSSGPDSTLSTYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                           GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS
                                                                                                                                                               GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS
                                                                                                                                                                                                                                                                                                                               120 AA;
                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0054452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-IB00207
                                                                                                                                                                                                                                                                      Score 588; DB; Pred. No. 4.1:
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doran JL,
                                                                                                                                                                                                                                                                       ; DB 15;
. 4.1e-48;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay WW;
            agfA fragment.
                                                                                                                                                                                                                                                                                                 Length 120;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                              112
                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                         0;
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Search completed: October 11, Job time: 33 secs
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                                                                                                                         Вр
                                                                                                                                                     Qy
                                                              Вb
                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 112; Conserv
                                                                                                                                                                                                                                                                                              The present sequence represents an agfA fragment encoded by an agfA gene fragment derived from Salmonella enteritidis 27655-3b TnphoA mutant strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules
                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 7; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated Salmonella gene agfA - u enteropathogenic bacteria of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-1994;
26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                                                                                                                                                                                                                                  from virtually all other microbial organisms.
                                                              61
                                                                           82 GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS 133
                                                                                                                                          22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                         1 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1997-309886/28.
                                                            GQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT74141
                                                                                                                                                                                                                                                      120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0233788
93US-0054452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9305-0054452
                                                                                                                                                                                76.1%; 5-
100.0%; Pro
0;
              2002, 21:13:17
                                                                                                                                                                                                   Score 588; DB 18;
Pred. No. 4.1e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used for diagnosis of Salmonella Enterobacteria family
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay WW;
                                                                                                                                                                                                                    Length 120;
                                                                                                                                                                                        Indels
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                              Score
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1: /cgn2_6/ptodata/2,
2: /ggn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                              Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    October 11, 2002, 21:12:43; Search time 17 Seconds (without alignments) 216.957 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
  11.5
10.55
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10.22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/Packfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                              Length DB
 US-08-233-788A-59
US-08-233-788A-57
US-08-233-788A-3
US-08-2447A-5
US-09-196-387-8
US-09-196-387-2
US-09-336-447A-13
US-09-336-447A-13
US-09-336-447A-13
US-09-336-447A-13
US-09-336-447A-13
US-08-808-59A-24
US-08-808-59A-24
US-08-808-29C-3
US-08-687-373-2
US-08-254-573-2
US-08-254-573-2
US-08-36-47A-7
US-08-254-573-2
US-08-36-47A-7
US-08-36-47A-7
US-08-36-47A-7
US-08-36-47A-7
US-08-581-739-4
US-08-172-332-1
US-08-172-332-1
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US-08-968-685A-10
US-08-038-682-2
US-08-302-832-2
                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231628
                    Sequence 59, Appli
Sequence 37, Appli
Sequence 3, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 204, Appli
Sequence 204, Appli
Sequence 24, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence
Sequence
Sequence
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1 MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

US-08-233-788A-59

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Query Match
Best Local Similarity

99.4%;

Score 768; DB 1; Lengum LL., Pred. No. 8.8e-68; uismatches 1; Indels

0; Gaps

0

60

Matches

150;

Conservative

TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids

ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92/
TELECOMMUNICATION INFORMATION:

920043.403C2

RESULT 1  US-08-233-788A-59  Sequence 59, Application US/08233788A  Patent No. 5635617  GENERAL INFORMATION:  APPLICANT: DOTAN, James L.  APPLICANT: Collinson, Karen S.  ANDERSOEE: Seed and Berry  STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle  STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle  STATE: Washington  COUNTRY: U.S.A.  ZIP: 98104-7092  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER FLORABLE PC-DOS/MS-DOS  SOFTWARE: PatentIn Release #1.0, Version #1.25  CURRENT APPLICATION NUMBER: US/08/233,788A  FILING DATE: 26-APR-1994  CLASSIFICATION: 435  APPLICATION: 435  APPLICATION: 435  APPLICATION: 435  APPLICATION: 435  APPLICATION: 435	28 77.5 10.0 1536 2 US-08-530-198-2 29 77.5 10.0 1536 2 US-08-469-880-2 30 77.5 10.0 1536 2 US-08-617-697-2 31 77.5 10.0 1536 2 US-08-617-697-2 31 77.5 10.0 1536 2 US-08-169-927-2 33 77.5 10.0 1612 1 US-08-199-20-7 34 77 10.0 1026 1 US-08-194-290-7 35 77 10.0 1026 2 US-08-614-377A-7 36 77 10.0 1026 4 US-09-142-648B-7 37 76.5 9.9 211 1 US-08-327-730-16 40 76.5 9.9 211 1 US-08-327-730-16 40 76.5 9.9 211 1 US-08-327-730-16 40 76.5 9.9 211 1 US-08-327-730-16 41 76.5 9.9 211 1 US-08-387-874-16 42 76.5 9.9 211 1 US-08-899-575-34 43 76.5 9.9 211 1 US-08-899-575-34 44 76.5 9.9 211 2 US-08-383-619-16 45 76.5 9.9 211 5 PCT-US93-08364-16
DETECTION	Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 34, Appl Sequence 36, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl

B

MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ

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RESULT 3
US-08-864-038A-3
; Sequence 3, Application US/08864038A.
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                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NNPALVNQTASDSSYMVRQVGFGNNATANQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 26-APR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 (CITY: Seattle
                                                                                                                                                                                           22 VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV 81
                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                      Local Similarity
les 112; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
                                                                                                                                                                           VVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08233788A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collinson, Karen S. Clouthier, Sharon C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6300 Columbia Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kay, William W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doran
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                          SEEDANBERRY ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHODS AND COMPOSITIONS FOR DETECTION OF SALMONELLA
                                                                                                                                                                                                                                                     76.1%; Score 588; DB 1; 100.0%; Pred. No. 2.3e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/233,788A
                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     920043.403C2
                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #1
                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                 Length 120;
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                        0;
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Qy В Ω 밁 Qy

US-09-336-447A-5

Sequence 5, Application US/09336447A
Patent No. 6310190
GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: AEBI, CHRISTOPH

AEBI, CHRISTOPH COPE, LESLIE D. MACIVER,

APPLICANT:

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US-08-864-038A-3
RESULT 4
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 8-
FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,31
REFERENCE/DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KUNIO NAK
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 1 FILING DATE: May 28, PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (212)986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                       504 LGGGSAAAAAAAAAAASGGGGRALRRALRRQMRGGGSAAA 543
                                                                                                                                                                                                         419 LLKSSASASASASASASAG-----GGGGGGGNGGGNGGGG-------GGGAGALA---- 460
                                                                                         118 YGGNNAALVNQTASDSS-----VMVRQVGFGNNATA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: Microsc SOFTWARE: Word Perfect 6
                                                                                                                                                                                                                                                                                                                                                                               LOCATION: from 1 to 738 IDENTIFICATION METHOD: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                   63 ARKSETTITQSGYGNGADVGQGADNSTIELTQ----NGFRNNATIDQWNAKNSDITVGQ 117
                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: peptide LOCATION: from 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                           3 LLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSD 62
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VENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
VENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
VENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
VENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBOD
VENTION: TO SAID POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212)953-7733
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27.5%;
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RESULT 5
US-09-196-387-8
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CURRENT FILING DATE: 199-06-21
NUMBER OF SEO ID NOS: 98
SOFTWARE: Patentin Ver: 2.1
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TYPE: PRT
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                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
           SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
                                                                                                          TELEPHONE: 201-487-5800
                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0
FILING DATE: June 10, 19
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Smith, Susan
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                                                       TELEFAX: TELEFAX: 133521
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                                                                                                                                             NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       FILING DATE:
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New Jersey
amino acid
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                                                                                      201-343-1684
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28.5%;
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Pred. No. 0.46;
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                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 949 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/0
FILING DATE: June 10, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                     MOLECULE TYPE:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
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APPLICANT: Smith,
                                                                                                                                                                                                                                                                                                       TELLEFAX: ZV_
TELLEFAX: 133521
Tex: 133521
158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
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                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
                               65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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nes 35; Conserv
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                                                                                                  VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA
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411 Hackensack Avenue,
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                                                                                                                                                 Score 92; DB 4
Pred. No. 0.77;
                                                                                                                                   Mismatches
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RESULT 7
US-09-196-387-2
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; HYPOTHETICAL:
US-09-196-387-2
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US-09-336-447A-13
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                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                Sequence 13, Application US/09336447A Patent No. 6310190
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Best Local Similarity
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APPLICANT: de Lan
APPLICANT: Smith,
                                                                      APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/0 FILING DATE: June 10, 19 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               158 GVSSTAPLGPGAAGPGTGVPAVSGALRELLEACRNGDVSRVKRLVDAANVNAKDM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 201 - 343 - 1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY:
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                                                                                                                                                                                                                                                                                                                                       99 VAAAPVVPAVSTSSAAGVAPNPAGSGSNNSPSSSSSPTSS-SSSSPSSPGSSLAESPEAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                  65 KSETTIT----QSGYGNGADVGQGADNSTIELTQNG--FRNNATIDQWNAKNSDI 113
                                                                                                                                                                                                                                                                                                                                                                        6 VAAFAAI-VVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDAR 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                    11.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 92; DB 4; Length 1327; Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Moraxella catarrhalis US-09-336-447A-13
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CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
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Best Local Similarity
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                               Query Match
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                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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APPLICANT: Dillon, Davin
TITLE OF INVENTION: COMPO
                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 943 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 LLIVGILGMATTASAQQTIARQ--GKGMHSIIGGGNDNEANGDYSTVSGGDYNEA----
Local Similarity hes 39; Conserv
                                                                                                                                                                                                                                     NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 07-APP
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                     STRANDEDNESS:
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                                                                                OPOLOGY:
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                                                                                                                     amino acid
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26.5%; Pred. No. 1.2;
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                   11.5%;
25.3%;
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                     Score 89; I
Pred. No. 1.
                                      DB 4;
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                                    Length 943;
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SEQ ID NO 9
LENGTH: 941
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-09-336-447A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
                                                                                                                                                                                                                                                                                                                     sequence 24, Application US/08808599A
Patent No. 6111089
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/336,447A CURRENT FILING DATE: 199-06-21 NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HANSEN,
APPLICANT: AEBI,
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                                                                                                                                                                                                                                                             APPLICANT: Fukuda, Michiko N. TITLE OF INVENTION: Trophinin, TITLE OF INVENTION: Proteins &
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                ADDRESSEE: Campbell
                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 QAKGEHSTIA--GGKN----NQATGNGSF---AAGVENKADAN 202
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                                                                                                                           STREET: 4370 La JC
CITY: San Diego
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 AQVVKTNNKKNGTHPFIGGGDYNTTKGNYPTIGGGHFNTAEGNYSTVGGGFTNEAIGKNS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
    OPERATING SYSTEM:
                        COMPUTER:
                                                                                           ZIP: 92122
                                                                                                             COUNTRY:
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COPE, LESLIE D.
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                                                                                                                                                                          E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                             USA
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                           Trophinin, Trophinin-Assisting Proteins and Methods to Inhibit Implantation
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Best Local (
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INFORMATION FOR SEQ ID NO:
                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI[DOS] Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE S'
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/317,522 FILING DATE: 04-OCT-1994 PRIOR APPLICATION DATA:
            FILING DATE: February 21, CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: NAME: Plant, Thomas, G.
                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1160 amino aci
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                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515 AISTSFSGVLNSSASFGGAIN----TSAGFGSTLN----SSASFGSALSTSASFGGVLN 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    566 GRAGFGGALNT-----NATFGGVLNGSAGFGGAMNTNATFG--GALNSNAGFGGAISTST 618
                                                                                                                                                                                                                                                                           STREET: LILLY CORPORTY: INDIANAPOLIS
STATE: IN
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                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 TQSGYGNGADVGQGADNSTIELTQNG-----FRNNATIDQWNAKNSDITVG----- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P-LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
REGISTRATION NUMBER:
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Pred. No. 12;
18; Mismatches
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US-08-737-716-2
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                                              ; MOLECULE TYPE: US-08-737-716-2
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Query Match
Best Local Similarity
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                                                                                                                         APPLICATION NUMBER: EP FILING DATE: 12-MAY-19 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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TOPOLOGY: unknown
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                    SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                          APPLICATION NUMBER: PCT/
FILING DATE: 12-MAY-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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Local Similarity 25.8%;
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                                                                                              TYPE:
                                                                                                                                                                                                                                                         FILING DATE: 22-APR-1997 CLASSIFICATION: 435
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                                                                              TOPOLOGY:
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                                                                                                             ENGTH:
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                                                                                                             437 amino acids
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VENTION: Process for the lysis of a culture of lactic
VENTION: acid bacteria by means of a lysin, and uses of the resulting
VENTION: lysed culture.
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Pred.
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                  Length 437;
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US-09-043-123-2
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US-08-209-747-8
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Best Local Similarity
Matches 37; Conserv
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                                                                                                                                                    Sequence 8, Application US/08209747 Patent No. 5733771
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APPLICANT: BLUM, Andre
APPLICANT: CORTHESY-THEULAZ, Irene
TITLE OF INVENTION: NEW ADHESIN FROM HELICOBACTER PYLORI
FILE REFERENCE: 05648004
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                                                                                                   GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Colgin, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 5
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                                                TITLE OF INVENTION: cDNAs Encodin TITLE OF INVENTION: Silk Proteins NUMBER OF SEQUENCES: 56
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                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             346 SSQVNAFNGFITKIGYKQFFGENKNVGLRYYGFFSYNGAGVGNGPTYNQ 394
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 STREET:
                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                    GPSGDSGAAAAFLDAALAQHVFNSANAGNDLSAKEFTSLVQNIVNNSQNALTLANNANIS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                    GGNHNGGGNSSGPDSTLSIYQYGSANA-----
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E: Birch, Stewart, Kolasch & Birch
P.O. Box 747
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                                                                                                                                                                                                                                                                                                   --GNNATANQ 150
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CITY: Falls Church

COUNTRY: Usania

COUNTRY: Usan

ZIP: 2040-3487

ZIP: 2040-3487

CONFUTER: IBM PC Compatible
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYRE: STEME PC COMPATION
COMPUTER READABLE FORM:
MEDIUM TYRE: PAPELLCATION LONG
SOFTMARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/209,747

FILING DATE: 14 MAR-1994

CLASSIFICATION: $30

ATTONNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 1447-104P

TELECHMUNICATION INFORMATION:
TELEPHONE: 703-205-8000

TELEPHONE: 703-205-8000

TELEPHONE: 703-205-8000

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TELEPHONE: 703-205-8000

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TELEPHONE: 103-205-8000
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2002 Compugen Ltd
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probable

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121 NNAALVNQTASDSSVMVRQVGFGNNATANQY

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?	Db 04 Db 45	Z 111 (C)	A; Ge C; Fu A; De A; No C; Ke F; 1- F; 21	A; Acco A; Sta A; Mol A; Res A; Not C; Gen	A A A A A A A A A A A A A A A A A A A	A; Re A; Re A; Cr	RESU JC60 fimb C;Sp C;Da C;Ac C;Ac		
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	SDARKS:	Match ocal Sim	r : in	Accession: A48898 Status: preliminar Molecule type: pro Moscules: 21-33 <c ext="" genetics:<="" note:="" sequence="" td=""><td>Molecule type: prote Residues: 21-52 <co2 173,="" 27658<="" 477="" a4="" authors="" bacteriol.="" collinson,="" contents:="" emo="" experimental="" note:="" number:="" purification="" reference="" s.k.;="" source:="" td="" the="" title:="" tr=""><td>Reference number: Recession: JC6039 Molecule type: DN Residues: 1-151 &lt; Cross-references: Accession: PC6015</td><td>protein s: Salmo 31-Dec-1 ion: JC6 son, S.K riol. 17</td><td></td><td>95.5 93.5 93.5 93.5 93.5 93.5 93.5 93.5</td></co2></td></c>	Molecule type: prote Residues: 21-52 <co2 173,="" 27658<="" 477="" a4="" authors="" bacteriol.="" collinson,="" contents:="" emo="" experimental="" note:="" number:="" purification="" reference="" s.k.;="" source:="" td="" the="" title:="" tr=""><td>Reference number: Recession: JC6039 Molecule type: DN Residues: 1-151 &lt; Cross-references: Accession: PC6015</td><td>protein s: Salmo 31-Dec-1 ion: JC6 son, S.K riol. 17</td><td></td><td>95.5 93.5 93.5 93.5 93.5 93.5 93.5 93.5</td></co2>	Reference number: Recession: JC6039 Molecule type: DN Residues: 1-151 < Cross-references: Accession: PC6015	protein s: Salmo 31-Dec-1 ion: JC6 son, S.K riol. 17		95.5 93.5 93.5 93.5 93.5 93.5 93.5 93.5
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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia A;Reference number: A64720; MUID:97426617
A;Accession: G64846
                                                                                                                                                                                                                                                                   A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 199 R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change
C;Accession: S70788; G64846; S31202; S34550; S34559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , S.; Moule, S.; O'Gaora, Nature 413, 848-852, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
A;Cross-references: GB:AB000205; GB:U00096; NID:g1787265; PIDN:AAC74126.1; A;Experimental source: strain K-12, substrain MG1655 R;Olsen, A.; Arnqvist, A.; Hanmar, M.; Sukupolvi, S.; Normark, S. mol. Microbiol. 7, 523-536, 1993
                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X90754; NID:g1147558; PIDN:CAA62282.1; PID:g1147564
A;Experimental source: strain K12, substrain W3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Microbiol. 18, 661-670, 1995
A; Title: Expression of two csg operons is
A; Reference number: S70783; MUID:96414468
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A; Residues: 1-151 <PAR>
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A; Residues: 1-151 <BLAT>
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                                                                                                                                                A; Status: nucleic acid sequence not shown;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG 120
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_AI0635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.; Bian, Z.; Olsen, A.; Normark,
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Davis, P.; Davies, R.M.; Dowd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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i, L.; White, N.
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                                                                          PID:g1787279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .; Churcher, N.; Farrar,
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DNA Res. 8, 11-22, 2001
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 21-42; 44-50 < OLS2>
R; Olsen, A.N.; Arnqvist, A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-6,'V',8-151 <OLS1>
A; Cross-references: EMBL:L04979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: The RpoS sigma factor relieves H-NS-mediated A;Reference number: S31202; MUID:93211294 A;Accession: S31202
                                                                                                                                                       A;Cross-references: GB:BA000007; PIDN:BAB34843.1; PID:g13360880; GSPDB:GN00154 A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                              curlin major subunit CsgA [imported] - C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: major component of wild-type curli; interaction between A;Note: curli are thin, coiled fibers expressed on the surface of Esch and H-kininogen; in the absence of CsgA, CsgB can self-assemble into F;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; MoLecule type: DNA
A; Residues: 1-133, 'RQRDSGWLW' <OLS3>
A; Cross-references: EMBL:LO4979; NID:g290424;
A; Experimental source: strain K-12, substrain
              Ωy
                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-152 <HAY>
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A; Accession: S34559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, October 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S34560
                                                                                                                                        A; Gene:
                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                        gasawara, N.;
                                                                                                                                                                                                                                                                                                                                                                               R; Hayashi, T.; Makino, K.;
                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: D90806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D90806
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113;
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                                                                              Local Similarity
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MKLLKVAAFAAIVVSGSALAGVVPQW-GGGGNHNGGGNSSGPDSTLSIYQYGSANAALAL
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                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                        K.; Ohnishi, M.; Kurokawa, K.; Ishii
T.; Kuhara, S.; Shiba, T.; Hattori,
                                                                            73.0%;
73.0%;
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Pred. No. 7e-41;
                                                                            Score 564.5; DB 2
Pred. No. 3.9e-39;
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                                                          Mismatches
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W3110
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QSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYG 119

MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNSELNIYQYGGGNSALAL

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A;Cross-references: GB:AL591985; PIDN:CAC49389.1; PID:g15140875; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                          R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: E95965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical glycine-rich protein [imported] - Sinorhizobium meliloti (strain 1021) maga
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: H85665
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A; Residues: 1-152 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ller, L.; Grotbeck, E.J. Nature 409, 529-533, 2001
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                           A; Gene:
                                           C; Genetics:
                                                                    A; Contents: annotation
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A; Residues: 1-2174 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: E95965
                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
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Pred. No. 3.9e-39;
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RESULT 7
S70787
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N;Alternate names: csgB protein; curlin nucleation component; mi
C;Species: Escherichia coli
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change
C;Accession: S70787; F64846
R;Hammar, M.; Arnqvist, A.; Bian, Z.; Olsen, A.; Normark, S.
Mol. Microbiol. 18, 661-670, 1995
A;Title: Expression of two csg operons is required for productio
A;Reference number: S70783; MUID:96414468
A;Accession: S70787
                                                                                                                                                                                                                                                                         A;Description: minor component of wild-type curli; interaction between CsgA and R;Note: curli are thin, coiled fibers expressed on the surface of Escherichia co and H-kininogen; in the absence of CsgA, CsgB can self-assemble into polymers F;1-21/Domain: signal sequence #status predicted <SIG>F;22-151/Product: minor curlin chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 277, 1453-1462, 1997
A;TitLe: The complete genome sequence of Escherichia
A;Reference number: A64720; MUID:97426617
A;Accession: F64846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: the nucleotide sequence was submitted to R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE000205; GB:U00096; NID:g1787265; PIDN:AAC74125.1; PID:g17872
A;Experimental source: strain K-12, substrain MG1655
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A; Residues: 1-151 <BLAT>
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A;Experimental source: strain K12, substrain W3110
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A; Residues: 1-151 <HAM>
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|| :|: | ||||| |||:| |; | |
AIATAGAGAVGILAQSIGGGGG----GGNATGGDAGFGSFQIGGGGGG-------73
                                                                                                                                      SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 97
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                                       RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                      AAGYDLANSEYNF----AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
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                                                                                                                                                                                                         Score 112.5; DB Pred. No. 0.023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the EMBL Data Library, Au Perna, N.T.; Burland, V.;
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subunit precursor CsgB [imported]

Escherichia

coli (strain O157:H7,

su

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gasawara, N.; Yasunaga, T.; Kuuqara, C., Sasawara, C., Sasawara
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C;Date: 18-Jul-2001 #sequen
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A; Residues: 1-151 <STO>
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Nature 409, 529-533, 2001
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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A; Residues: 1-151 <HAY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNNATIDQWNAKNSDITVGQYGGNNAALVNQTASDSSYMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF 97
                                                                                                                                                                                                                                                                                                                                                                 SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity
35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 112.5; DB Pred. No. 0.023;
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Shiba, T.; Hat
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anta, E.;
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G
      A; Reference number:
A; Accession: S42136
A; Molecule type: DNF
                                                                 submitted to the EMBL Data A; Reference number: $42136
                                                                                                                               R; Taylor, F.M.; Martindale, D.W.
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nucleation component of curlin monomers [imported] - Salmonella enterica subsp. ();Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: AH0635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Description: minor c
A:Note: fimbriae bind
cnjB protein - Tetrahymena thermophila
C;Species: Tetrahymena thermophila
C;Date: 19-Mar-1997 #sequence_revision
C;Accession: S42136; S42135; S03650
                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-151 < PAR>
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                                                                      RESULT
S42136
                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
A; Gene: STY
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Authors: Parry, C.; Quail, M.; Rutherford, K.; A;Title: Complete genome sequence of a multiple A;Reference number: AB0502; PMID:11677608 A;Accession: AH0635
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                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AL513382; PIDN:CAD08267.1; PID:g16502314; GSPDB:GN00176
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                                                                                                                                          EGENNRAKVDQ---AGNYNFAYIEQTGNANDASISQSAYGNSAAIIQKGSGNKANITQY
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36; Conserv
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Davis, P.; Davies, R
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tissue plasminogen
                    #text_change 07-Dec-1999
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F;1451-1464/Region: zinc finger CCHC mc
F;1478-1491/Region: zinc finger CCHC mc
F;1501-1514/Region: zinc finger CCHC mc
F;1530-1543/Region: zinc finger CCHC mc
F;1559-1568/Region: zinc finger CCHC mc
F;1579-1592/Region: zinc finger CCHC mc
F;1602-1615/Region: zinc finger CCHC mc
                                                                                                                                                                        Connor, R.; Davies, R.; Devlin, K.; Feltwell, T. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; A;Title: Decliphering the biology of Mycobacterium A; Reference number: A70500; MUID:98295987
A;Accession: F70825
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  A; Gene: PPE
C; Superfamily:
                                                           A;Cross-references: GB:AL021958; GB:AL123456; NID:g3261536; PIDN:CAA17522.1; A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                   R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H
                                                                                                                                                                                                                                                                                                                                                   probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul1-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jan-2000
C;Accession: F70825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Genetic code: SGC5
A;Introns: 85/3; 136/1;
C;Keywords: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 236-250, 'I', 252-255, 'N', 257-773
A; Cross-references: EMBL: X06462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Martindale, D.W.; Taylor, F.M.
Nucleic Acids Res. 16, 2189-2201, 1988
A;Title: Multiple introns in a conjugation-specific gene
A;Reference number: S03650; MUID:88189811
A;Accession: S03650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1164-1174;1179-1198;1233-1252;1285-1293;1297-1309;1316-1326;1331-1341;1343
A; Cross-references: EMBL:L03710
                                               C; Genetics:
                                                                                                          A; Molecule type: DNA
A; Residues: 1-645 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Retroviral-type zinc A; Reference number: $42135; MU A; Accession: $42135
                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: cnjB
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A; Cross-references: EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 21, 4610-4614, 1993
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 FGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QWGGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV•81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -SGSGNQ----TGGGWGSN---DNQQQQNENTGGGGWGSSNS----NQTNNESS-----
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unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Martindale,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136/1; 157/3; 201/2;
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  collagens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID:g161751; PID:g161752
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motiff
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motiff
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---CQSNVQES-TTTSSGGWGS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                 Whitehead, S.; Barrell, B.G. tuberculosis from the complete
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RESULT 14
H98144
                                                      A;Title: The Genome of the Natural Genetic A;Reference number: AB2577; PMID:11743193 A;Accession: AD3143
                                                                                                                                                                                          conserved hypothetical protein Atu4768 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AD3143 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wooderse, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: A97359; PMID:11743194
A;Accession: H98144
A;Stature
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A; Molecule type: DNA
A; Residues: 1-145 <KUR>
                                        A;Status: preliminary
                                                                                                                     ster, E.W.
                                                                                                                                      Science 294, 2317-2: A; Authors: Yoo, H.;
                                                                                                                                                                                                                                                                                                                  AD3143
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A; Residues: 1-145 < KUR>
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A.; Liu, F.; Wollam, C.; Al
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision
C;Accession: H98144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein AGR_L_228 [imported] - Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                              Karp,
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                                                                                                                                 P.; Romero, P.; Zhang, S.
294, 2317-2323, 2001
rs: Yoo, H.; Tao, Y.; Biddle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                GOYGGNNAALVNOTASDSSVMVRQVGFGNNATANQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLKVAAFAAIVVSGSALAGVVPQWGG-----GGNHNGGGNSSGPDSTLSIYQYGSANA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNTGNNNIGIGLTGSNQIGFGGLNSGSGNIGFGNSGTGN 384
                                                                                                                                                                                                                                                                                                                                                                                             GQFGSNHTTILTQDGNGNIAAGVQVGRGCSANVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV 115
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37; Conser
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                                                                                                                               Tao,
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C.; Allinger, M.; Doughty, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -HQYGRHNLSAVGQEGHDNYGSTTQNGNRNVAGI-
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Pred. No. 0.29; 
17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 105.5; Di Pred. No. 0.08;
                                                                                                                               P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                               Engineer
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                                                                                               Agrobacterium tumefaciens C58
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A;Cross-references: GB:AE008689; PIDN:AAL45562.1; PID:g17743277; GSPDB:GN00187

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A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu4768
A;Map position: linear chromosome
A;Map linear chromosome
A;Map
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RESULT 15
Q98LN6
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Search completed: October 11, 2002, 21:14:22 Job time : 30 secs
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STRAIN-MARF303099;

MEDLINE-21082930; PubMed-11214968;

Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,

Watanabe A., Idesawa K., Ishikawa A., Kawashina K., Kimura T.,

Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,

Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,

Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the nitrogen-fixing symbiotic bacterium

Mesorhizobium loti.";

DNA Res. 7:331-338(2000).

EMBL: AP002996; BAB48427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 3659 AA;
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
MLL0950 PROTEIN.
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NCBI_TaxID=381;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 AALVNOTASDSSVM 136
                                                                                                                                                                                                                          107 NAKNSDI---TVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                                                                                                                                                                                                                                 375 GNNSQGILAQTIGGGGGDGGSNFGLFASGGS---GSLG-GNGGPAN 416
                                                                                                                                                                                                                                                                                              323 IYSHGIAAQSIGGGGGGSAGGFGLFSSSGGSG---GNGGNGGIVQVT-----NNANIATW 374
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                                                                                                                                                                                                                                                                                                                                                              IYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGFRNNATIDQW 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Mismatches
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RESULT 12
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                                                                                                                 RESULT 13
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Best Local S
Matches 40
                                                                     Q9KKB1;
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Nature 393:537-544(1998).
EMBL; 282098; CAB05045.1; -. Tuberculist; Rv3533c; -.
                          01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Pfam; PF00823; PPE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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               OMPB
                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
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InterPro; IPR000030; PPE.
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            (FRAGMENT).
                                                                                                                                                                                                                                                                                                            VPQWGGG--GNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGAD
                                                                                                                                                             IGAGNTGSSNWGFGNNGIGN 312
                                                                                                                                                                                                                                                                                LPNLGIGNIGNANLGGGNTG-DLNTGNGNIGNTNLGSGNRGDANLGSGNIGNSNVG-GGN 232
                                                                                                                                                                                         ---SSVMVRQVGFGNNATAN 149
                                                                                                                                                                                                                       VGNGNFGSGNGRAGLPGSGNVGNGNLGNSNLGSGNTGNSNVGFGNTGNNNVGTGNAGSGN 292
                                                                                                                                                                                                                                                   VGQ---GADNSTIEL-----TQNGFRNNATIDQWNAKNSDITVGQYGGNNAALVNQTASD 132
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582 AA; 55503 MW; B895BDD55979A9C6 CRC64;
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                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                      PRELIMINARY;
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28.6%;
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19,
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Pred. No. 4.6;
14; Mismatches
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Query Match
Best Local
                                                               Submitted (MAY-1999) to the E
EMBL; AC007357; AAD31072.1; -
InterPro; IPR005504; RRM.
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20393643; PubMed=10939649;
Roux V., Raoult D.;
"Phylogenetic analysis of members of the genus Rickettsia using gene coding the outer-membrane protein rompB (ompB).";
Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
EMBL; AF123713; AAF34116.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia japonica.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                             STRAIN-CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lee J.M., Len:
Vysotskaia V.S., Schwartz J.R., Luros J., Ngan I., Gonzalez A.,
Liu S., Li J., Kremenetskaia I., Luros J., Ngan I., Gonzalez A.,
Altafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P.,
Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walk
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome 1 BAC F3F19 sequence.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       O9SAF2;
01-mAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
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                                         SEQUENCE
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                                                                                                                                                        STRAIN=CV.
                                                                                                                                                                     SEQUENCE FROM N.A.
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Similarity
                                                        PS50102; RRM; 1
                                         573 AA;
                                                                                                                                                        COLUMBIA;
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                                          61400 MW;
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13.2%;
26.1%;
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Last sequence update)
Last annotation updat
                                                                                                                            EMBL/GenBank/DDBJ databases
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Pred. No. 18;
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CSGB...
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EMBL: AL021988; CAA17522.1; "...
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053818;
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Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Pred. No. 3.1
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EMBL; AJ131756; CAB45377.1; -.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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RV3159C OR MTV014.03C
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EMBL; AL021646; CAA16624.1; -.
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InterPro; IPR000030;
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FGNSGNNNIGFFNSG-NNNVGFFNSGNNNFGFGNAGD
                                               WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGA
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37; Conser
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29.8%;
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Last annotation updat
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                                                                                                                    Score 105;
Pred. No. 4.
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                                                                                                 46;
  - INTGFGNAGDTNTGF
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Best

27.0%;

Pred. No. 4.7;

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RESULT
O93397
ID 099
AC 099
AC 090
DT 011
DT 011
DT 011
DT 012
CS CCC
OC ECC
OC AC
CC SC CC
RP SE
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                                                                                          093397;
093397;
01-NOV-1998
01-NOV-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998
01-JAN-1998
01-DEC-2001
                                HYOSOPHORIN.

Cyprinus carpio (Common carp).

Eukaryota; Metazoa; Chordata; Craniata;

Actinopterygii; Neopterygii; Teleostei;

Cypriniformes; Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        033801
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE ....
MEDLINE-98053981; Pubmec ...
MEDLINE-1" S.S., Lorentz R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGFB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             033801;
  SEQUENCE FROM N.A
                      NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                              cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella typhimurium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella typhimurium
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                                                                                                                                                                                                                                                                                                                                                                                                      Infect.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
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                                                                                                                                                                                             AVVVQKQSHMAIRVTQ 178
                                                                                                                                                                                                                     ALVNQTASDSSVMVRQ 139
                                                                                                                                                                                                                                            GNSAAI---
                                                                                                                                                                                                                                                                 GNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITV------GQYGGNNA 123
                                                                                                                                                                                                                                                                                       GSKLLSVISQ-ERGGNNRAKVDQAGNYNFAYIEQTGNAN------DASISQSAY 109
                                                                                                                                                                                                                                                                                                             GSALAGYVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGGNGGAGGEVSVSLTDSAIRTGQGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITQSGYGNGADVG------QGADNSTI--ELTQNGFRNNATIDQWNAK---NSDITV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIATAGAGAVGILAQSIGGGGGN----GGNATGGDAGFGSFQIGGGGGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIVVSGSALAGVVPQ--WGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSET
                                                                                                                                                                                                                                                                                                                                                                                          AJ000514;
                                                                                                                                                                                                                                                                                                                                    1 Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   Immun. 65:5320-5325(1997).
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Gremblrel.
(Tremblrel.
                                                                                                                                                                                                                                                                                                                                                                                179 AA;
                                                                                        (TrEMBLrel. 08,
(TrEMBLrel. 08,
(TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               CAA04150.1; -.
va; 19318 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9393832;
orentz R.G., Gordon J.I.,
                                                                                                                                                                                                                                            -SAAIIQKGSGNKANITQYGTQKTAVVVQKQSHMAIQANITQYGTQKT 162
                                                                                                                                                                                                                                                                                                                                              14.1%;
27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                           aggregative fimbriae promotes interaction um SR-11 with mouse small intestinal epithe
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19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma
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Last annotation updat
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Last sequence update)
Last annotation update)
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                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179
                                                                                                                                       348 AA
                                                        Vertebrata;
                                              Euteleostei;
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                                                                                          update)
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                                                                                                                                                                                                                                                                                                                                                       Length 179;
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                                                        Euteleostomi;
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                                              Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                          epithelial
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                                                                                         Query Match
Best Local S
Matches 39
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Best Local :
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                                                                                                                                                                                                                                SMART; SM003
Zinc-finger.
CONFLICT
1640
                                                                                                                                                                                     CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            094821; p92146; p92145; p92144; p92143; p92142; p92141; 01-FEB-1997 (TIEMBLIFE). 02, Created) 01-FEB-1997 (TIEMBLIFE). 02, Last sequence update) 01-DEC-2001 (TIEMBLIFE). 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsao C.C., Huang F.L., Chang Y.S.;
"Purification, characterization, and hyosophorin.";
Mol. Reprod. Dev. 52:288-296(1999).
EMBL; AF077819; AAC27329.1; -
SEQUENCE 348 AA; 33164 MW; 4CEAE1
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Retroviral-type zinc fingers and glycine-rich repeats encoded by cnjB, a Tetrahymena gene active during meios Nucleic Acids Res. 21:4610-4614(1993).
                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 21:4610
EMBL; X06462; CAB37323.1;
EMBL; L03710; AAC37171.1;
HSSP; P05888; 1AAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Multiple introns thermophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=88189811; PubMed=3357771;
Martindale D.W., Taylor F.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetrahymenina; Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetrahymena thermophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNJB PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q94821
                                                                                                                                                                                                                                                                                                      PRINTS;
                                                                                                                                                                                                                                                                                                                            Pfam; PF00098; zf-CCHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taylor F.M., Martindale D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94051569; PubMed=8233798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5911;
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                                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                           25
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                                           QWGGGGNHNGG---GNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADV
QFGGGGNSNGGQSWGTSSGSDWN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSGSNGTMTQDDGSGSNATTTRDDGSGSNGTTTR----DDGSGSNGTTTQDDGSGSNATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSALAGVVPQWGGGGNH-----NGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETT1
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                                                                                                                                                                                                                                                                            SM00343; ZnF_C2HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                         Similarity 30.1
39; Conservative
                                                                                                                                                                                                                                                                                                         PR00939;
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                                                                                                                                                                                     251
256
1748 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                      C2HCZNFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in a conjugation-specific
                                                                                                                                                                                     251 M -
256 I -
199624 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16:2189-2201(1988)
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27.4%;
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                                                                                           20;
                                                                                         Score 108; DB Pred. No. 8.5; Pred. No. 8.5; 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 108.5;
Pred. No. 1.
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                                                                                                                                                                                  -> I (IN REF. 1).
-> N (IN REF. 1).
-> OB03F210104008A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligohymenophorea; Hymenostomatida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1748 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Γ.3;
  -CQSNVQES-TTTSSGGWGS----
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Bacteria; Proteobacteria;
Escherichia.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-43895 RED VARIANT; MEDLINE-21218556; PubMed-11319125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                        EMBL; U53207; AAA98671.1; -
                                                                                  Cox J.M., Eglezos S., Woolcock J.B.; "Virulence of Salmonella enteritidis in chickens correlates colony morphology and expression of SEP17 fimbriae."; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                          STRAIN-SE30
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                     Salmonella.
                                                                                                                                                                             Salmonella enteritidis.
Bacteria; Proteobacteria;
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Pred. No. 2e-
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            Score 385; DB 2;
Pred. No. 1.3e-21
                                          2FD5411241A7BCB1 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
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HYPOTHETICAL GLYCINE-RICH PROTEIN SMB21548.
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EMBL; AJ131756; CAB45380.1; -.
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Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision;
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                                         "The complete sequence of the 1,683-kb pSymB megaplasmid fixing endosymbiont Sinorhizobium meliloti."; proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
                                                                                     MEDLINE-21396508; PubMed-11481431;
Finan T.M., Weidner S., Wong K., Buhrmester
Vorhoelter F.J., Hernandez-Lucas I., Becker
Golding B., Puehler A.;
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                       SEQUENCE
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

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# SUMMARIES

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	homo	095271 homo sapien	Q9vbc4 drosophila	Q19414 caenorhabdi	Q9kka5 rickettsia	Q90wr5 lampetra fl	Q9xyd8 hirudo medi		Q	Q9sia8 arabidopsis	drosophi	Q9xcj4 salmonella	Q9kx38 moraxella c	Q92g62 rickettsia		ש	065937 mycobacteri	P95248 mycobacteri	(I)	S	002402 pinctada fu		2		P96840 mycobacteri	Q9ngf6 drosophila	Q9ngf7 drosophila	Q9bit1 plectreurys	Q9kka8 rickettsia	

## ALIGNMENTS

O33802 PRELIMINARY; PRE O33802; O33802; O1-JAN-1998 (TrEMBLrel. 05, Last 01-JAN-1998 (TrEMBLrel. 19, Last 01-DEC-2001 (TrEMBLRE); gamma samments of the salmonella typhimurium sr-11 with 11-Salmonella typhimurium sr-11 with cells."; Expression of thin, aggregative salmonella typhimurium sr-11 with cells."; Profest. Immun. 65:5320-5325(1997) Infect. Imm	Db Oy	Qy Db	Qu Be Ma	SQ.	RL DR	RT	RT	RA	R R P	RN C	Q 8	8	20	E E	D,	֓֞֞֞֜֞֓֓֓֞֞֞֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	AC	ij	RESULT 033802	
PRT; 152 AA.  Created) Last sequence update) Last annotation update) Last annotation update)  3832; Gordon J.I., Bian Z., Pfeifer J.D., tive fimbriae promotes interaction of with mouse small intestinal epithelial 1997) 9DA7DADC2364B006 CRC64; Score 764; DB 2; Length 152; Pred. No. 4.9e-49; Pred. No. 4.9e-49; Score 764; DB 2; Length 152; Pred. No. H.9e-49; 1; Mismatches 1; Indels 0; Gaps 0; POWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ 60	SDARKSETTITOSGYGNGADVGGGADNSTIELTONGFRNNATIDUWNAKNSDITVGQYGG 	MKLLKVAAFAAIVVSGSALAGVVPQWGGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQ	8%; Score 764; DB 2; Length 152; 7%; Pred. No. 4.9e-49; 1; Mismatches 1; Indels 0; Gaps	NON_TER 152 152 SEQUENCE 152 AA; 15401 MW; 9DA7DADC2364B006 CRC64;	Infect. Immun. 65:5320-5325(1997). EMBL; AJ000514; CAA04151.1;	Salmonella typhimurium SR-11 with mouse small intestinal epithelial cells.":	"Expression of thin, aggregative fimbriae promotes interaction of	z R.G., Gordon J.I., Bian Z., Pfeifer	SEQUENCE FROM N.A. MEDLINE-98053981; PubMed-9393832;	NCBL_1dxID=602; [1]	Salmonella,	la; gamma subdivision;	Salmonella typhimurium.	AGFA PROTEIN (FRAGMENT).	(TrEMBLrel. 19,	(Tremburel 05,		33802 PRELIMINARY; PRT; 152	RESULT 1	

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Search completed: October 11, 2002, 21:13:42 Job time: 13 secs
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Riede I., Drexler K., Eschbach M.L., Henning U.;
Riede I., Drexler K., Eschbach M.L., Henning U.;
Phase sequence of genes 38 encoding a receptor-recognizing protein of bacterLophages T2, K3 and of K3 host range mutants.";
J. MOL. BLOL. 194:31-39(1987).
J. FUNCTION: VG38 IS AT THE TIP OF THE LONG TAIL FIBERS AND SERVES AS THE PHAGE RECOGNITION SITE FOR THE CELLULAR RECEPTOR.

AS THE PHAGE RECOGNITION SITE FOR THE CELLULAR RECEPTOR.

AS THE STREET OF THIS PHAGE USE OUTER MEMBRANE PROTEINS OMPF AND TTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                    Fiber protein; Phage recognition. SEQUENCE 262 AA; 25801 MW; 0567366918F6C745 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X05312; CAA28935.1; -. PIR; S00275; S00275.
                                                                                                                                                                                                   175 GGGGRPFGVGGKIGSDSILS----GSNASL---TDAGTGGTTF-QYGAGNGGNVGAGGG 225
                                                                                                      226 -----RGWGKNVYTSEGGAAGAAVT 245
                                                                                                                                                                                                                               27 GGGGNHNGGGNSSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGAD 86
                                                                                                                                                     87 NSTIELTQNGFRNNATIDQWNAKNSDIT 114
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"The rickettsial outer membrane protein A and B genes of Ricke australis, the most divergent rickettsia of the spotted fever Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OMPB_RICCN STANDARD; PRT; 1655 AA.

Q9KKA3; Q9KK98; Q9XC45;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Outer membrane protein B precursor (188 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide
OMPB OR RC1085.
                                                                                                                      SEQUENCE OF 353-1655 FROM STRAIN=Malish 7;
                                                                                                                                                                                                                                                                                                                                                                                                            Samson D., Roux V., Raoult D.;
                                                                       "The rickettsial outer membrane
                                                                                                 Stenos
                                                                                                                                                                                    "Phylogenetic analysis of members of gene coding the outer-membrane proteint. J. Syst. Evol. Microbiol. 50:144
                                                                                                                                                                                                                                                                            STRAIN-Indian tick typhus, and Malish MEDLINE-20393643; PubMed-10939649;
                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 33-1649 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rickettsiaceae; Rickettsieae; NCBI_TaxID=781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                                                                                                                                                                                                                      "Mechanisms of evolution in Science 293:2093-2098(2001).
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vol. Microbiol. 50:1449-1455(2000)
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LMKCTYKI -> FEVYI (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                   iffren P., Fournier P.-E., Weissenbach J., Claverie
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No. 6
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Viruses; dsDNP
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SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURAL PROTEIN WHICH MAY PLAY VIRULENCE FACTOR AND/OR IMMUNOGEN SIMILARITY).
FUNCTION: THE 32 KDA BETA PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
SUBCELLULAR LOCATION:
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                                                                                                                                                                                                                                                                                                                                       NAKNSDIT---VGQYGGNNAAL-----VNQTASDSSVMVRQVGFGNN
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AF123721; AAF34124.1;
AF123726; AAF34129.1;
AF149110; AAD39533.1;
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120 KDA SUBFACE-EXPOSED PROTECTION CONTROL OF CONTROL 
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in Gp38).
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IN INDIAN TICK TYPHUS).
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P20469;
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PIR; JQ0188; JQ0188.
HSSP; P06620; IINA.
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01-FEB-1991 (Rel. 17, Last sequ
16-0CT-2001 (Rel. 40, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILINE-90092494; PubMed-2599095;
Abe K., Watabe S., Emori Y., Watanabe M., Arai S.;
Nah ice nucleation active gene of Erwinia ananas. Sec
to those of Pseudomonas species and regions required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleation activity.";
FEBS Lett. 258:297-300(1989).
                                                                                                                                         between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                             CRYSTALLIZATION IN SUPERCOOLED WATER.
SUBCELLULAR LOCATION: Outer membrane (By similarity).
DOMAIN: CONTAINS MANY IMPERFECT REPEATS OF THE CONSENSUS
OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: ICE NUCLEATION PROTEINS
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                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                     There are no restrictions ong as its content is in
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01-FEB-1996
01-NOV-1997
                                                                                                                                                                                                                      Rieger M., Brueckner M., Schaefer M., "Sequence analysis of 203 kilobases fr chromosome VII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X17316; CAA351
PIR; S07053; S07053.
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PROSITE; PS00314; ICE_NUCLEATION; 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
    between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1014 SSQTARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P49687;
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                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                    YEAST 13:1077-1090(1997).
-!- FUNCTION: MAY PLAY A DIRECT ROLE IN NUCLEOCYTOPLASMIC EXPORT RNA AND ALSO IN PROTEIN IMPORT. BINDS HOMOPOLYMERIC RNA.
                                                                                                                                                                                                                                                                                                                                                                                                            "NUP145 encodes a novel yeast glycine-leucine-phenylalanine-glycine (GLFG) nucleoporin required for nuclear envelope structure.";
J. Cell Biol. 125:955-969(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 26109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homopolymeric RNA in v
Cell 78:275-289(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=94320139; PubMed=8044840; Fabre E., Boelens W.C., Wimmer C., Mattaj I.W., Hurt E.C.; Fabre E., Boelens W.C., wimmer export of mRNA and binds "Nupl45p is required for nuclear export of conserved motif."; homopolymeric RNA in vitro via a novel conserved motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=94320139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94253246;
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                                                                                                           DOMAIN: CONTAINS G-L-F-G REPEATS.
       European
                                                                                                 SIMILARITY: BELONGS TO THE GLFG FAMILY OF NUCLEOPORINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QNGFRNNATIDQWNAKNSDITVGQYG-----GNNAALV----NQTASDSSVMVRQVGFG 143
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                           the Swiss Institute
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1322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 33, Created)
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PubMed=8195299,
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W; 89B0EE24AA837039 CRC64;
                             of Bioinformatics
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EMBL; X75780; CAA53406.1; -.
EMBL; Z8068; CAA61905.1; -.
PIR; B44402; B44402.
PIR; S39173; S39173.
PIR; S44518; S44518.
SGD; S0001551; NUP100.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94264407; PubMed=7764866; Michigami Y., Watabe S., Abe K., Obata H., Ar "Cloning and sequencing of an ice nucleation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-KUIN-3;
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Bacteria; Proteobacteria; gamma su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for com
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                                                                                                                                                                                                                                            FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUC
CRYSTALLIZATION IN SUPERCOOLED WATER.
SUBCELLULAR LOCATION: Outer membrane.
DOMAIN: CONTAINS IMPERRECT REPEATS OF A CONSENSUS OCTAPE
A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL
PERIODICITY IS SUPERIMPOSED.
                                                                                                                                                      MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF IC SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGNHNGGGNSSGPDSTLSIY--QYGSANAALALQSDARKSETTITQSGYGN-----GA 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Biotechnol. Biochem.
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571 29 x 6 AA APPROXIMATE REPEATS
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  This SWISS-PROT entry is copyright. It is produced throubetween the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its contenmodified and this statement is not removed. Usage by
                                                                                                                                                                                                                                                                                     CRYSTALLIZATION IN SUPERCOOLED WATER.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- DOMAIN: CONTAINS 126 IMPERFECT REPEATS OF A C
A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  herbicola, Pseudomonas fluorescens and Gene 85:239-242(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The consensus sequence of ice nucleation proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Warren G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=M1
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                                                                                                                                                                                                                                                                                                                                                                                                   -1- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90152370; PubMed=2515997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=549;
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DOMAIN 162 993 OCTAPEPTID
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Pfam; PF00818; Ice_nucleation; 51.
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                                                                                                                                                                                      PERIODICITY IS SUPERIMPOSED.

MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF IC SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv1548c.
RV1548C OR MT1599 OR MTCY48.17.
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Q10778;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                             laboratory strains.";
Submitted (APR-2001) to
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                      Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                          STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98295987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Actinomycetales;
                                                                      This
                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 NNNN----NNNGGQTSMMGHPF-YGGNPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105
                                                                                                                                                                             Whole genome comparison of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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      European Bioinformatics Institute. Tr
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                                             SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the En
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38, Last sequence up
40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=9634230;
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ZINC FINGERS.
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A -> R (IN REF. 2).
M; D7068BB2BC0F6F77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GGGCTGNGGGGASGPGGGPSANSGGGGGGG-----
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                             restrictions
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                                                      EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                   Q02629;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Nucleoporin NUP100/NSP100 (Nuclear pore protein
NUP100 OR NSP100 OR YKL068W OR YKL336
                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; 'TRANSMEM 14 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002989; Mycobact_pentapep
InterPro; IPR000030; PPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rubercuList; Rv1548c;
                       KNOWN PICTEINS.";

Yeast 10:S69-S74(1994).

YEAST 10:S69-S74(1994).

YEAST 10:SESENTIAL COMPONENT OF NUCLEAR PORE COMPLEX.

YEAST OF NUCLEOPORINS MAY BE INVOLVED IN BOTH BINDING AND TRANS

THE PROTEINS DURING NUCLEOCYTOPLASMIC TRANSPORT.

YES SUBCELLULAR LOCATION: NUCLEAR PORE COMPLEX.

YES DOMAIN: CONTAINS G-L-F-G REPEATS.

YES SIMILARITY: BELONGS TO THE GLFG FAMILY OF NUCLEOPORING.
                                                                                                                                                                                                                                                  MEDLINE-93054906; PubMed-1385442; Wente S.R., Rout M.P., Blobel G.; Wente New family of yeast nuclear pore J. Cell Biol. 119:705-723(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N100_YEAST
                                                                                                                             "Sequence of a 20.7 kb region of yeast chromosome XI includes the NUP100 gene, an open reading frame (ORF) possibly representing a nucleoside diphosphate kinase gene, tRNAs for His, Val and Trp in addition to seven ORFs with weak or no significant similarity to
                                                                                                                                                                                                  MEDLINE-94378724;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
 This
                                                                                                                                                                                 Rasmussen S.W.;
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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 SWISS-PROT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                  PubMed=8091863;
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28.0%;
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Pred. No.
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D -> G (IN REF. 2).
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                            FAMILY OF NUCLEOPORINS
                                                                                                                                                                                                                                                                   complex proteins.";
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                                                                                  TRANSLOCATION
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     collaboration
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RESULT 6
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Best Local :
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   OVO_DROME STANDARD;
P51521; Q9XZU4;
01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICEMUCLEATIN.
PROSITE; PS00314; ICE_NUCLEATION; 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P06620;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xanthomonas campestris pv. translucens.";
Mol. Gen. Genet. 223:163-166(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-X56S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1990
01-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91080859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conserved repetition in the ice nucleation gene inax
                                                                                                                                  318
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                                                                                                                                                                                                                                                                                   205
                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                                                    14 VSGSALAG-----VVPQWGG----GGNHN------GGGNSSGPDSTLSIYQYGSANAALAL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 se SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ittes requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleation;
UENCE 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRYSTALLIZATION IN SUPERCOOLED WATER.
SUBCELLULAR LOCATION: OUTCE membrane (By Similarity).
DOMAIN: CONTAINS 153 IMPERFECT REPEARS OF THE CONSENSUS
OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE IC
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gen. Genet. 223:163-166(1990).
FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleation
                                                                                                                                                             ---DQWNAKNSDITVGQYG-----GNNAALV-----NQTASDSSVMVRQVGFGNNATANQ
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                                                                                                                                  YGSTQTARKGSDITAG-YGSTGTAGSDSALIAGYGSTQTAGSESSLT--AGYGSTQTARK 374
                                                                                                                                                                                                       STLTAGYGSTQTAQEGSRLTSGYGSTAT---SGSDSAVI----SGYGSTQTAGSESSLTAG
                                                                                                                                                                                                                                                                                 VYGSTLTGADQSRLVAGYGSTETAGDHSDLIAGYGSTGTAGSDSSI-LAGYGSTQTAAGR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X52970; CAA37140.1; -.
                                                                                                                                                                                                                                                                                                                                                          49;
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AA; 15;
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16, Last
40, Last
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                                                                                                                                                                                                                                                                                                                                                                          13.1%; 27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                               at; Outer membrane.
152548 MW; C8B451
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                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00048; ZINCFINGER. SMART; SM00355; ZnF_C2H2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000822; znf-C2H2.
Pfam; PF00096; zf-C2H2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U11383; AAB60216.1;
EMBL; X59772; CAB36921.1;
HSSP; P25490; 1ZNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The European Bioinformatics Institutions as long use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mevel-Ninio M.T.M., Terracol R., Kafatos F.C.;
"The ovo gene of Drosophila encodes a zinc finger protein required for female germ line development.";

EMBO J. 10:2259-2266(1991).

1- FUNCTION: REQUIRED FOR SURVIVAL AND DIFFERENTIATION OF FEMALE GERM LINE CELLS. PLAYS A ROLE IN GERM LINE SEX DETERMINATION.

-1- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Garfinkel M.D., Wang J., Liang Y., Mahowald A.P.; "Multiple products from the shavenbaby-ovo gene region melanogaster: relationship to genetic complexity."; Mol. Cell. Biol. 14:6809-6818(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ovo protein (Shaven OVO OR SVB.
                                                                                                                                                                                                                                                                                                                                                                                         Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0003028;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95021209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE: FIRST APPEARS IN THE GERMARIUM AND ACCUMULATES IN NURSE CELLS DURING OOGENESIS. STORED IN THE BUT IS RAPIDLY LOST IN THE EMBRYOS EXCEPT FOR ITS CONTINUED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRESENCE IN THE GERM LINE PRECURSOR POLE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    melanogaster (Fruit fly).
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-- T . Liang Y., Mahowald A.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34, Last sequence update) 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=1712294;
 baby protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                           DNA-binding;
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POLY-GLN.
POLY-GLN.
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                                                                                                                                                                                                                                                                                                                                                                                           Repeat; Nuclear protein;
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CSGB_SALTY
P55226;
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01-OCT-1996
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR 2002 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17
CSGB OR AGFB OR STM1143.
                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Courtney L., Porwollik S., Ali J., Darke M., Du F., Hou Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., w Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nha Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella typhimurium, and Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=S.enteritidis; STRAIN=270
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Romling U., Bian 2., Hammar M., Sierralta W.D., Normark "Curli fibers are highly conserved between Salmonella ty Escherichia coil with respect to operon structure and re J. Bacteriol. 180:722-731(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-S.typhimurium; STRAIN-SR-MEDLINE-98117058; PubMed-9457880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision;
                                                                                                     SEQUENCE
                                                                                                                                                            StyGene;
                                                                                                                                                                             EMBL; U43280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                              Fimbria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fimbriae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collinson S.K., Clouthier S.C., Doran J.L., Banser salmonella enteritidis agfBAC operon encoding thin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome
              51
                                                                                                                                                                                                                                                                                                                                                                                     BACTERIO1. 178:662-667(1996).

FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AND COLLED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: STRONG, TO E.COLI CSGB
                                                                                                                                                                                                                                                                                                                                                                          CURLIN MONOMERS.
GSANAALALQSDARKSE-----TTITQSGYGNGADVGQ-GADNST-----
                                                                                                                                                                                           AJ002301; CAA05316.1; -. AE008749; AAL20073.1; -.
                                          1 Similarity
36; Conserv
                                                                                                                  Signal; Complete proteome
1 21 POTEN
22 151 MINOR
                                                                                                                                                            SG10609; csgB
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151 AA;
                                           Conservative
                                                                                                                                                                          AAC43598.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Salmonella
                                                                                                     WW.
                                                                                                   POTENTIAL.
MINOR CURLIN SUBUNI
; C0FC5430E6DD361D
                                                         Score 111.5;
Pred. No. 0.
                                           Mismatches
                                                                                                                  CURLIN SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enterica serovar Typhimurium
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                                                                                                                                                                                                                                                                                                                  a collaboration
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Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rompB)
(romp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMPB_RICJA STANDARD; PRT; 16
006653;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Uchiyama T.;
"Sequencing of the gene encoding the protein japonica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen;
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
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-i- FUNCTION: THE 120 KDA SUFFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-YH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rickettsiaceae; Rickettsieae;
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Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB003681; BAA20138.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003858; rOmpA_rOmpB;
                                                105
                                                                                                                                                                                             509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: CELL WA LAYER WITH HEXAGONAL SYMMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE
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01-OCT-1996 (Rel. 34, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Minor curlin subunit precursor.
CSGB OR B1041 OR Z1075 OR ECS1419.
Escherichia coli, and
Escherichia coli 0157:H7.
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                                                 Sampei G.,
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MEDLINE=97426617; PubMed=9278503;
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                                       T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., O K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., K., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
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Arngvist A., Olsen A., Normark S.;
Sigma S-dependent growth-phase induction of the csgBA promoter in Escherichia coll can be achieved in vivo by sigma 70 in the absence of the nucleoid-associated protein H-NS.";
Mol. Microbiol. 13:1021-1032(1994).

-i-FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AR COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
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"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
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[6]
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                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                Fimbria;
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Hayashi T., Makino K., Ohnishi M., Kurokawa
Han C.-G., Ohtsubo E., Nakayama K., Murata '
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MEDLINE=21074935; PubMed=11206551;
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[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding to the 12.7 DNA Res. 3:137-155(1996).
                                 98
 77
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                RNNATIDQWNAKNSDITYGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY
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SNRAKIDQTGDYNL-AYIDQAGSANDASISQGAYGNTAMIIQKGSGNKANITQY
                                                                                             SSGPDSTLSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGADNSTIELTQNGF
                                                                                                                                                                                                                                                                                           AE000205; AAC74125.1; -. D90741; BAA35831.1; -. AE005315; AAG55787.1; -.
                                                                                                                                                                                                                                                                                                                                             X90754; CAA62281.1;
                                                                                                                                                                                                                                                                           AP002554; BAB34842.1; -.
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35; Conserv
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Signal; Complete proteome.
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                                                                                                                                Conservative
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                                                                                                                                                                                             15882 MW;
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                                                              AVNELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGS
                                                                                                                               13;
                                                                                                                                              Score 112.5;
Pred. No. 0.
                                                                                                                                                                                                              MINOR CURLIN SUBUNIT.
                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                            B18D266B964014B8 CRC64;
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T., Tanaka
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Tobe T.,
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RESULT 2
CSCA_ECOLI
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DT 01-OEC
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or send a
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-:- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
-:- COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY A'
TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Doran J.L., Collinson S.K., Burian J., Sarlos G., 7 Munro C.K., Kay C.M., Banser P.A., Peterkin P.I., I "DNA-based diagnostic tests for Salmonella species the structural gene for thin, aggregative fimbriae J. Clin. Microbiol. 31:2263-2273(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Purification and characterization Salmonella enteritidis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91310586; PubMed=1677357
Collinson S.K., Emoedy L., Muell
                         Major
CSGA (
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Bacteria;
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                                                                                                                                                             NNAALVNQTASDSSVMVRQVGFGNNATANQY 151
                                                                                                                                                                                                                        SDARKSETTITOSGYGNGADVGQGADNSTIELTQNGFRNNATIDQWNAKNSDITVGQYGG
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  Proteobacteria;
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B7DAC0D16B621359
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                                                                                                                                                                                                                                                                                                                                                                                                MAJOR CURLIN SUBUNIT.
                                                                                                                                                                                                                                                                                                                      Score 773;
Pred. No. 5
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  subdivision;
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  Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                  Length
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Kay W.W.;
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., I
Ikemoto K., Inada T., Itoh T., Kajihanda M., Kanai K.
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nisl
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., M. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A.,
                                                                                                                                                                                    J. Bacteriol. 173:4773-4781(1991).

-:- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. COILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO
                                                                                                                                                                                                                                                                    SEQUENCE OF 21-31.

MEDLINE=91310586; PubMed=1677357;

COllinson S.K., Emoedy L., Trust T.J., Kay W.W.;

"Purification and characterization of thin, aggregative
                                                                                                                                                                                                                                                                                                                                                Arnqvist A., Olsen A., Pfeifer J., "The Crl protein activates cryptic fibronectin binding in Escherichia Mol. Microbiol. 6:2443-2452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=K12 / YMEL;
MEDLINE=93023873; PubMed=1357528;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 21-40.
STRAIN-K12 / YMEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A 718-kb DNA sequence of the Escherichia coli K-12 corresponding to the 12.7-28.0 min region on the lir DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sampei G., Seki Y., T
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96414468; PubMed=8817489;
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Escherichia coli.";
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              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
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SIMILARITY:
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Kajihara M., Kanai K., Kashimoto K.,
K., Masuda S., Miki T., Mizobuchi K.
Y., Nashimoto H., Nishio Y., Saito N
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gene of fibronectin-binding c
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N145_YEAST
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OMPB_RICJA
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MBN_DROME
YM96_YEAST
HYR1_CANAL
Y136_TREPA
ILF3_HUMAN
SGG_DROME
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ICEV_PSESX
YKO3_CAEEL
ICEN_PSEFL
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escherichia
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## ALIGNMENTS

RP RX RA	RR RT	RA RA	RARA	R R R R R R R R R R R R R R R R R R R	R R R R R R R R R R R R R R R R R R R	800000	CSGA AC DT DT DT DT	RESULT
SEQUENCE FROM N.A. SPECIES=S.enteritidis; STRAIN=27655-3B; MEDLINE=96146512; PubMed=8550497; Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.; "Salmonella enteritidis agfBAC operon encoding thin, aggregative	genome sequenoserovar Typhi os:848-852(2001)	Feitwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;	RAIN-CT18;  bbed=11677608;  G., James K.D., Thomson N.R., Pickard D., Wa G., James K.D., Holden M.T.G., Sebainia K.L., Bentley S.D., Holden M.T.G., Sebainia Brooks K., Chillingworth T., Connerton P., Davies R.M., Dowd L., White N., Farrar J., Pares R.M., Dowd L., White N., Farrar J., N., Davies R.M., Dowd L., White N., Farrar J., Pares R.M., Pare	MEDLINE=2154948; PUDMed=1167/509; MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2."; Nature 413:852-856(2001). [3] SEQUENCE FROM N.A.	SEQUENCE FROM N.A.  SPECIES=S.typhimurium; STRAIN=SR-11;  SPECIES=S.typhimurium; STRAIN=SR-11;  MEDLINE=98117058; PubMed=9457880;  Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;  Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;  Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;  Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;  Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;  Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;  Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;  Seguence From N.A.  Species=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;	Salmonella typhimurium, Salmonella typhi, and Salmonella enteritidis. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella. NCBI_TaxID-602, 601, 592;	A_SALTY A_SALTY CSGA_SALTY CSGA_SALTY STANDARD; PRT; 151 AA.  P55225; 01-CCT-1996 (Rel. 34, Created) 01-CCT-1996 (Rel. 34, Last sequence update) 01-MR-2002 (Rel. 34, Last annotation update) Major curlin subunit precursor (Fimbrin SEF17). CSGA OR AGFA OR STM1144 OR STV1181.	11.00 1